**BLASTP 2.2.9 [May-01-2004]****Reference :**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1088011356-16594-155894407553.BLASTQ4

**Query=**

(532 letters)

**Database:** All non-redundant GenBank CDS

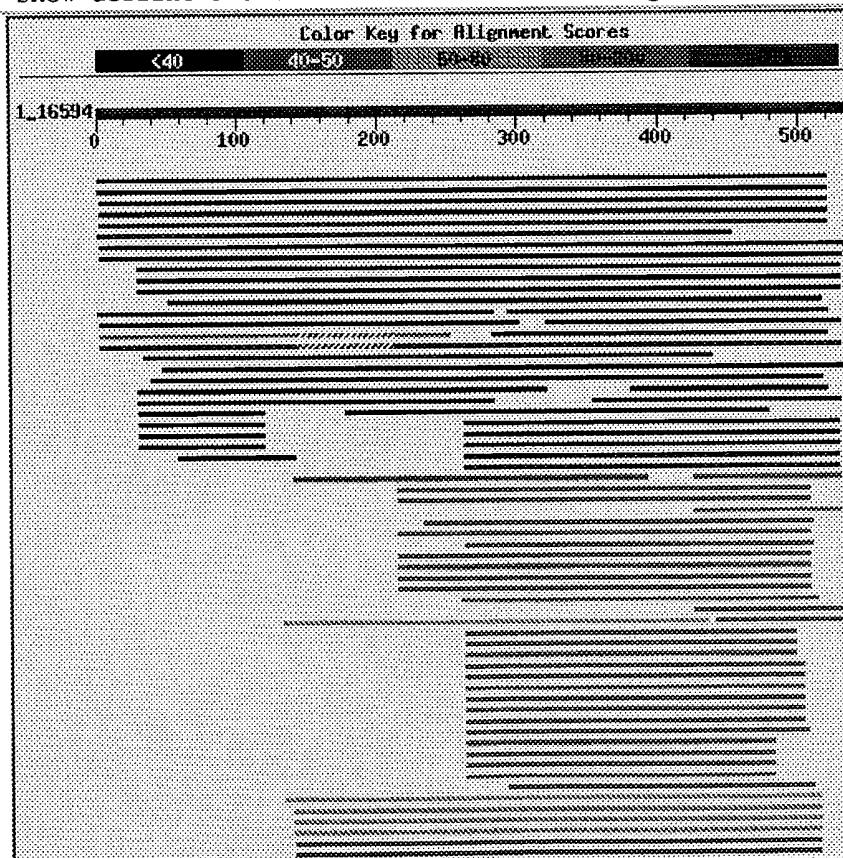
translations+PDB+SwissProt+PIR+PRF excluding environmental samples  
1,866,121 sequences; 619,474,291 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

**Distribution of 103 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:			Score (bits)	E Value	
gi 40255141 ref NP_060841.3		chondroitin beta1,4 N-acetylga...	1075	0.0	
gi 22852208 dbj BAC16217.1		beta-1,4-N-acetylgalactosaminy...	1074	0.0	
gi 26348685 dbj BAC37982.1		unnamed protein product [Mus mu...	1002	0.0	
gi 31559877 ref NP_766341.2		RIKEN cDNA 4732435N03; beta1,4...	1001	0.0	
gi 26324624 dbj BAC26066.1		unnamed protein product [Mus mu...	1001	0.0	
gi 9651083 dbj EAB03554.1		hypothetical protein [Macaca fas...	915	0.0	
gi 34877724 ref XP_224757.2		similar to chondroitin beta1,4...	828	0.0	
gi 47219910 emb CAF97180.1		unnamed protein product [Tetrao...	720	0.0	
gi 24429592 ref NP_061060.3		chondroitin beta1,4 N-acetylga...	665	0.0	
gi 31560032 ref NP_084441.3		chondroitin sulfate GalNAcT-2 ...	659	0.0	
gi 26386533 dbj EAB31761.2		unnamed protein product [Mus mu...	657	0.0	
gi 47227595 emb CAG09592.1		unnamed protein product [Tetrao...	577	e-163	
gi 38174240 gb AAH60772.1		ChGn protein [Homo sapiens]	557	e-157	
gi 26340498 dbj BAC33912.1		unnamed protein product [Mus mu...	532	e-150	
gi 7023813 dbj BAA92093.1		unnamed protein product [Homo sa...	523	e-147	
gi 20072996 gb AAH26599.1		4732435N03Rik protein [Mus muscu...	494	e-138	
gi 34858369 ref XP_232316.2		similar to chondroitin beta1,4...	486	e-136	
gi 47216537 emb CAG04715.1		unnamed protein product [Tetrao...	485	e-135	
gi 31198419 ref XP_308157.1		ENSANGP00000021559 [Anopheles ...	382	e-105	
gi 34365000 emb CAE46036.1		hypothetical protein [Homo sapi...	361	2e-98	
gi 24652379 ref NP_610567.1		CG12913-PA [Drosophila melanog...	351	2e-95	
gi 11360289 pir T46919		hypothetical protein DKFZp762L037.1...	317	5e-85	
gi 18677088 dbj EAB85092.1		unnamed protein product [Homo s...	317	5e-85	
gi 34365310 emb CAE45982.1		hypothetical protein [Homo sapi...	314	3e-84	
gi 37805317 gb AAH60169.1		Galnact2 protein [Mus musculus]	264	4e-69	
gi 47201472 emb CAF87906.1		unnamed protein product [Tetrao...	221	3e-56	
gi 37573674 dbj BAC98832.1		chondroitin sulfate synthase [H...	207	5e-52	
gi 42657278 ref XP_373440.2		chondroitin sulfate synthase 3...	207	5e-52	
gi 41529141 emb CAE17326.1		chodroitin synthase 2 [Homo sap...	207	6e-52	
gi 27681143 ref XP_225912.1		similar to carbohydrate (chond...	206	1e-51	
gi 28411190 emb CAD43233.1		chondroitin synthase 2 [Homo sa...	206	1e-51	
gi 7959793 gb AAF71068.1		PRO0082 [Homo sapiens]	195	2e-48	
gi 38086850 ref XP_194358.2		similar to mKIAA0990 protein [...	192	2e-47	
gi 37360174 dbj BAC98065.1		mKIAA0990 protein [Mus musculus]	192	2e-47	
gi 18606381 gb AAH23112.1		Galnact2 protein [Mus musculus]	191	3e-47	
gi 47086685 ref NP_997843.1		carbohydrate (chondroitin) syn...	187	5e-46	
gi 47213615 emb CAF95956.1		unnamed protein product [Tetrao...	186	9e-46	
gi 40789012 dbj BAA76834.2		KIAA0990 protein [Homo sapiens]	186	9e-46	
gi 15617453 dbj BAB64936.1		chondroitin synthase [Homo sapi...	186	1e-45	
gi 31542309 ref NP_055733.2		carbohydrate (chondroitin) syn...	185	2e-45	
gi 37182181 gb AAQ88893.1		CHSY1 [Homo sapiens]	185	2e-45	
gi 34857503 ref XP_218759.2		similar to carbohydrate (chond...	183	7e-45	
gi 41210270 ref XP_210054.3		similar to dJ341D10.1 (novel p...	174	3e-42	
gi 48139301 ref XP_396991.1		similar to chondroitin synthas...	174	3e-42	
gi 42662609 ref XP_378128.1		similar to dJ19N1.1 (novel pro...	149	2e-34	
gi 31158517 gb AAO85275.1		chondroitin synthase-like protei...	136	1e-30	
gi 45555191 ref NP_996440.1		CG9220-PC [Drosophila melanoga...	136	1e-30	
gi 45555180 ref NP_996439.1		CG9220-PB [Drosophila melanoga...	135	2e-30	
gi 31158514 gb AAO85273.1		chondroitin disaccharide polymer...	134	6e-30	
gi 31044074 dbj BAC76780.1		chondroitin synthase [Caenorhab...	134	6e-30	
gi 31158515 gb AAO85274.1		chondroitin disaccharide polymer...	134	6e-30	
gi 17509239 ref NP_492630.1		chondroitin disaccharide polym...	134	7e-30	
gi 33300399 emb CAE17977.1		C. elegans SQV-5 protein (corre...	133	9e-30	

gi 39595217 emb CAE60254.1	Hypothetical protein CBG03828 [...]	129	2e-28
gi 31200511 ref XP_309203.1	ENSANGP00000005393 [Anopheles ...]	122	2e-26
gi 34867122 ref XP_342818.1	similar to chondroitin betal,4...	100	1e-19
gi 38566700 ref NP_942585.1	beta 1,4-N-acetylgalactosaminy...	94	7e-18
gi 21757529 dbj EAC05141.1	unnamed protein product [Homo s...	91	6e-17
gi 38566692 ref NP_775864.2	beta 1,4-N-acetylgalactosaminy...	91	6e-17
gi 47077041 dbj BAD18454.1	unnamed protein product [Homo s...	91	8e-17
gi 34861210 ref XP_219477.2	similar to hypothetical protei...	87	1e-15
gi 24416540 gb AAH38881.1	BC038881 protein [Mus musculus]	87	1e-15
gi 40789265 ref NP_848632.2	betal,4-N-acetylgalactosaminy...	86	2e-15
gi 46275756 dbj BAD15101.1	betal,4-N-acetylgalactosaminy...	86	2e-15
gi 16553708 dbj BAB71566.1	unnamed protein product [Homo s...	85	3e-15
gi 9239926 dbj BAB00632.1	Not6 [Ciona intestinalis]	84	1e-14
gi 47210467 emb CAF94230.1	unnamed protein product [Tetrao...	74	9e-12
gi 47217479 emb CAG10248.1	unnamed protein product [Tetrao...	69	3e-10
gi 37181931 gb AAQ88769.1	RASL651 [Homo sapiens]	67	8e-10
gi 47215238 emb CAG01130.1	unnamed protein product [Tetrao...	65	3e-09
gi 27545323 ref NP_078812.2	chondroitin polymerizing facto...	65	4e-09
gi 12053139 emb CAB66748.1	hypothetical protein [Homo sapi...	64	7e-09
gi 10439162 dbj BAB15449.1	unnamed protein product [Homo s...	60	1e-07
gi 39644837 gb AAH08878.2	CHPF protein [Homo sapiens]	60	2e-07
gi 23594326 ref XP_129886.2	DNA segment, Chr 1, Brigham & ...	59	4e-07
gi 48525359 ref NP_001001565.1	chondroitin polymerizing fa...	59	4e-07
gi 27685255 ref XP_237306.1	similar to chondroitin polymer...	57	1e-06
gi 47224136 emb CAG13056.1	unnamed protein product [Tetrao...	53	2e-05
gi 28972740 dbj BAC65786.1	mKIAA1402 protein [Mus musculus]	46	0.002
gi 34853978 ref XP_216063.2	similar to mKIAA1402 protein [...]	45	0.003
gi 18043971 gb AAH19714.1	2010209012Rik protein [Mus muscu...	45	0.004
gi 17554378 ref NP_498934.1	putative protein, with a coile...	42	0.031
gi 32565140 ref NP_871671.1	putative cytoplasmic protein, ...	42	0.049
gi 39585100 emb CAE62751.1	Hypothetical protein CBG06915 [...]	41	0.076
gi 19922240 ref NP_610946.1	CG8536-PA [Drosophila melanoga...	40	0.17
gi 34857950 ref XP_227406.2	similar to Lbcl1 protein [Ratt...	39	0.24
gi 28958144 gb AAH47275.1	Similar to RIKEN cDNA 2010209012...	39	0.32
gi 5305592 gb AAD41721.1	N-acetylglucosamine galactosyltra...	39	0.34
gi 26006191 dbj BAC41438.1	mKIAA0651 protein [Mus musculus]	39	0.36
gi 47271404 ref NP_032513.2	rho/rac guanine nucleotide exc...	39	0.37
gi 13879244 gb AAH06589.1	Rho/rac guanine nucleotide excha...	39	0.37
gi 29421290 gb AAO59307.1	kinesin [Gibberella moniliformis]	39	0.44
gi 15792460 ref NP_282283.1	putative two-domain glycosyltr...	38	0.61
gi 47227208 emb CAG00570.1	unnamed protein product [Tetrao...	37	1.2
gi 40353014 gb AAH64509.1	CSGlcA-T protein [Homo sapiens]	37	1.3
gi 42657991 ref XP_376724.1	KIAA1402 protein [Homo sapiens...	37	1.4
gi 48717495 ref NP_061888.1	chondroitin sulfate glucuronyl...	37	1.4
gi 7243185 dbj BAA92640.1	KIAA1402 protein [Homo sapiens]	37	1.4
gi 45383942 ref NP_990534.1	beta-1,4-galactosyltransferase...	37	1.6
gi 24372098 ref NP_716140.1	NAD(P)H-flavin reductase [Shew...	37	1.6

## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|40255141|ref|NP\_060841.3| chondroitin betal,4 N-acetylgalactosaminyltransf  
sapiens]

gi|19352192|dbj|BAB85992.1| chondroitin betal,4 N-acetylgalactosaminyltransf  
sapiens]

gi|37182006|gb|AAQ88806.1| MMVR656 [Homo sapiens]

Length = 532

Score = 1075 bits (2780), Expect = 0.0

Identities = 521/521 (100%), Positives = 521/521 (100%)

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 Sbjct: 1 MMMVRRGLLAWISRVVLLVLLCCAI SVLYMLACTPKGDEEQLALPRANSPTGKEGYQAV 60

Query: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120  
 Sbjct: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120

Query: 121 LAFLHSQVDKAEVNAGVKLATEYA AVPFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDEL 180  
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Query: 181 VEAIESALET LN NPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240  
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Query: 241 LFRPFSPIMKV KNEKLN MANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300  
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Query: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKR 480  
 Sbjct: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKR 480

Query: 481 CMDELTP EQYKMC MQSKAMNEASHGQLGMLVFRHEIEAHLR 521  
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 >gi|22852208|dbj|BAC16217.1| beta-1,4-N-acetylgalactosaminyltransferase [Homo  
 Length = 532

Score = 1074 bits (2777), Expect = 0.0

Identities = 520/521 (99%), Positives = 520/521 (99%)

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 Sbjct: 1 MMMVRRGLLAWISRVVLLVLLCCAI SVLYMLACTPKGDEEQLALPRANSPTGKEGYQAV 60

Query: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120  
 Sbjct: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120

Query: 121 LAFLHSQVDKAEVNAGVKLATEYA AVPFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDEL 180  
 Sbjct: 121 LAFLHSQVDKAEVNAGVKLATEYA AVPFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDEL 180

Query: 181 VEAIESALET LN NPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240  
 Sbjct: 181 VEAIESALET LN NPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240

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Sbjct: 241 LFRPFGPIMKVKNELNMANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300

Query: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360  
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Sbjct: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360

Query: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD 420  
 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD

Sbjct: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD 420

Query: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGFHLWHEKR 480  
 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGFHLWHEKR

Sbjct: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGFHLWHEKR 480

Query: 481 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521  
 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR

Sbjct: 481 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521

☐ >gi|26348685|dbj|BAC37982.1| unnamed protein product [Mus musculus]  
 Length = 530

Score = 1002 bits (2590), Expect = 0.0

Identities = 477/521 (91%), Positives = 496/521 (95%), Gaps = 4/521 (0%)

Query: 3 MVRRLGLAWISRVVLLVLLCCAISVLYMLACTPKGDDEQLALPRANSPTGKEGYQAVLQ 62  
 MVRRLGL WISRVV+LLVLLCCAISVLYMLACTPKGD+EQL LPRAN PTGK+GYQAVLQ

Sbjct: 1 MVRRLGLGWISRVVILLVLLCCAISVLYMLACTPKGDQEQGLPRANGPTGKDGYQAVLQ 60

Query: 63 EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGL--GLDRSPPEKTQADL 120  
 E EEQHRNYV+SLKRQIAQLK+ELQ RSEQ R+GQ QASDA L G DR P K QADL

Sbjct: 61 EREEQHRNYVNSLKRQIAQLKDELQARSEQFRSGDQASDATSLRSGWDREP--KAQADL 118

Query: 121 LAFLSQVDKAEVNAGVKLATEYAAVPPDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 180  
 LAF L QVDKAEV+AGVKLATEYAAVPPDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL

Sbjct: 119 LAFRLRGQVDKAEVHAGVKLATEYAAVPPDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 178

Query: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240  
 VEAIESALE+LN+P E+SP+ RPYTA+DFIEGIYRTERDKGTLYELTFKGDHKHEF+RL+

Sbjct: 179 VEAIESALESLSNPVESP HQRPYTAADFIEGIYRTERDKGTLYELTFKGDHKHEFQRLV 238

Query: 241 LFRPFGPIMKVKNELNMANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300  
 LFRPF PIMKV K EKL N+ANTLINVIVPLA+RVDKFR FMQNFREMC I+QDGRVHLTVVY

Sbjct: 239 LFRPFGPIMKVKEKLNLAN TLINVIVPLARRVDKFRHFMQNFREMC IQDGRVHLTVVY 298

Query: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360  
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Sbjct: 299 FGKEEMNEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 358

Query: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD 420  
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Sbjct: 359 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGVIYGHHDVAPP LQQQLVIKKETGFWRD 418

Query: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGFHLWHEKR 480  
 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGFHLWHEK

Sbjct: 419 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGFHLWHEKH 478

Query: 481 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521  
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Sbjct: 479 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 519

☐ >gi|31559877|ref|NP\_766341.2| RIKEN cDNA 4732435N03; beta1,4 N-acetylgalactosa  
 [Mus musculus]

gi|26329203|dbj|BAC28340.1| unnamed protein product [Mus musculus]  
 Length = 530

Score = 1001 bits (2588), Expect = 0.0

Identities = 476/521 (91%), Positives = 496/521 (95%), Gaps = 4/521 (0%)

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 MVRRLGL WISRVV+LLVLLCCAISVLYMLACTPKGDE+EQL LPRAN PTGK+GYQAVLQ  
 Sbjct: 1 MVRRLGLGWISRVVILLVLLCCAISVLYMLACTPKGDEQLGLPRANGPTGKDGQAVLQ 60

Query: 63 EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGL--GLDRSPPEKTQADL 120  
 E EEQHRNYV+SLKRQIAQLK+ELQ RSEQ R+GQ QASDA L G DR P K QADL  
 Sbjct: 61 EREEQHRNYVNSLKRQIAQLKDELQARSEQFRSGQDQASDATSLRSGWDREP--KAQADL 118

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 180  
 LAFL QVDKAEV+AGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL  
 Sbjct: 119 LAFLRGQVDKAEVHAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 178

Query: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTYELTFKGDHKHEFKRLI 240  
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 Sbjct: 179 VEAIESALESVNSPVESSPHQRPYTAADFIEGIYRTERDKGTYELTFKGDHKHEFQRLV 238


Query: 241 LFRPFSPIMKVKNEKLNMAANTLINIVVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300  
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Query: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360  
 FGKEE+NEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD  
 Sbjct: 299 FGKEEMNEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 358

Query: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVPPLEQQLVIKKETGFWRD 420  
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 Sbjct: 359 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGVIYGHHDVPPPLGQQLVIKKETGFWRD 418

Query: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLSNLIIVVTRTPVRGLFHLWHEKR 480  
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 Sbjct: 419 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLSNLIIVVTRTPVRGLFHLWHEKH 478

Query: 481 CMDELTPQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLR 521  
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 Length = 530

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Identities = 476/521 (91%), Positives = 496/521 (95%), Gaps = 4/521 (0%)

Query: 3 MVRRLGLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ 62  
 MVRRLGL WISRVV+LLVLLCCAISVLYMLACTPKGDE+EQL LPRAN PTGK+GYQAVLQ  
 Sbjct: 1 MVRRLGLGWISRVVILLVLLCCAISVLYMLACTPKGDEQLGLPRANGPTGKDGQAVLQ 60

Query: 63 EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGL--GLDRSPPEKTQADL 120  
 E EEQHRNYV+SLKRQIAQLK+ELQ RSEQ R+GQ QASDA L G DR P K QADL  
 Sbjct: 61 EREEQHRNYVNSLKRQIAQLKDELQARSEQFRSGQDQASDATSLRSGWDREP--KAQADL 118

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 180  
 LAFL QVDKAEV+AGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL  
 Sbjct: 119 LAFLRGQVDKAEVHAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 178

Query: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTYELTFKGDHKHEFKRLI 240  
 VEAIESA+E+LN+P E+SP+ RPYTA+DFIEGIYRTERDKGTYELTFKGDHKHEF+RL+  
 Sbjct: 179 VEAIESAMESLNSPVESSPHQRPYTAADFIEGIYRTERDKGTYELTFKGDHKHEFQRLV 238


Query: 241 LFRPFSPIMKVKNEKLNMAANTLINIVVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300  
 LFRPF PIMKVK EKN+ANTLINIVVPLA+RVDKFR FMQNFREMCI+QDGRVHLTVVY  
 Sbjct: 239 LFRPFGPIMKVKKEKLNLANLANTLINIVVPLARRVDKFRHFMQNFREMCIQDGRVHLTVVY 298

Query: 301 FGKEEINEVGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360  
 FGKEE+NEVGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD  
 Sbjct: 299 FGKEEMNEVGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 358

Query: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD 420  
 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPG+IYGHHDVAPPPL QQLVIKKETGFWRD  
 Sbjct: 359 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGVIYGHHDVAPPPLGQQLVIKKETGFWRD 418

Query: 421 FGFGMTCQYRSDFINIGGFDDLKGWGGEDVHLYRKYLHSNLIVVRTPVRLGFHLWHEKR 480  
 FGFGMTCQYRSDFINIGGFDDLKGWGGEDVHLYRKYLHSNLIVVRTPVRLGFHLWHEK  
 Sbjct: 419 FGFGMTCQYRSDFINIGGFDDLKGWGGEDVHLYRKYLHSNLIVVRTPVRLGFHLWHEKH 478

Query: 481 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521  
 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR  
 Sbjct: 479 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 519

 >gi|9651083|dbj|BAB03554.1| hypothetical protein [Macaca fascicularis]  
 Length = 453

Score = 915 bits (2364), Expect = 0.0  
 Identities = 443/453 (97%), Positives = 448/453 (98%)

Query: 1 MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDDEQLALPRANSPTGKEGYQAV 60  
 MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGD+EQLALPRANSPTGKEGYQA+  
 Sbjct: 1 MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDDEQLALPRANSPTGKEGYQAI 60

Query: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120  
 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLG DRSPPEKTQADL  
 Sbjct: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGPDRSPPEKTQADL 120

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 180  
 LAFLHSQVDKAEV+AGVKL TEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL  
 Sbjct: 121 LAFLHSQVDKAEVHAGVKLTTEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 180


Query: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240  
 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRL+  
 Sbjct: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLV 240

Query: 241 LFRPFSPIMKVKNELNMANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300  
 LFRPF PI+KVK EKLNMANTLINVIVPLAKRVDKF QFMQNFREMCIEQDGRVHLTVVY  
 Sbjct: 241 LFRPFGPIIKVKEKELNMANTLINVIVPLAKRVDKFWQFMQNFREMCIEQDGRVHLTVVY 300

Query: 301 FGKEEINEVGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360  
 FGKEEINEVGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD  
 Sbjct: 301 FGKEEINEVGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360

Query: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD 420  
 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD  
 Sbjct: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD 420

Query: 421 FGFGMTCQYRSDFINIGGFDDLKGWGGEDVHL 453  
 FGFGMTCQYRSDFINIGGFDDLKGWGGEDVHL  
 Sbjct: 421 FGFGMTCQYRSDFINIGGFDDLKGWGGEDVHL 453

 >gi|34877724|ref|XP\_224757.2| similar to chondroitin beta1,4 N-acetylgalactosa  
 [Rattus norvegicus]  
 Length = 617

Score = 828 bits (2139), Expect = 0.0  
 Identities = 395/448 (88%), Positives = 417/448 (93%)

Query: 3 MVRRLGLLAWISRVVLLVLLCCAISVLYMLACTPKGDDEQLALPRANSPTGKEGYQAVLQ 62  
 MVRRLGL+ WISRVV+LLVLLCCAISVLYMLACTPKGD+EQL LPRAN PTGK+GYQAVLQ  
 Sbjct: 1 MVRRLGLVGWISRVVILLVLLCCAISVLYMLACTPKGDQEQLGLPRANGPTGKDGQAVLQ 60

Query: 63 EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLA 122  
E EEQHRNYV+SLKRQIAQLK+ELQ RSEQLR+GQ QASDA L P K QAD+LA  
Sbjct: 61 EREEQHRNYVNSLKRQIAQLKDELQARSEQLRSGQDQASDATSLRSGWDPEPKAQADILA 120

Query: 123 FLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEEKPVKDKRDELVE 182  
FL QVDKAEV+AGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEEKPVKDKRDELVE  
Sbjct: 121 FLRGQVDKAEVHAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEEKPVKDKRDELVE 180

Query: 183 AIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTYELTFKGDHKHEFKRLILF 242  
AIESALE+LN+P E+SP+ RPYTA+DFIEGIYRTERDKGTYELTFKGDHKHEF+RL+LF  
Sbjct: 181 AIESALESLSNPVLESSPHQRPYTAADFIEGIYRTERDKGTYELTFKGDHKHEFQRLVLF 240

Query: 243 RPFSPIMKVKNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFG 302  
RPF PIMKVK EKLNMANTLINVIVPLA+RVDKFR FMQNFREMCI+QDGRVHLTVVYFG  
Sbjct: 241 RPFGPIMKVKKEKLNMAANTLINVIVPLARRVDKFRHFMQNFREMCIQDGRVHLTVVYFG 300

Query: 303 KEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIY 362  
KEE+NEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNV+LFFCDVDIY  
Sbjct: 301 KEEMNEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVVLLFFCDVDIY 360

Query: 363 FTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFG 422  
FTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIYGHHDV LEQQLVIKKETGFWRDFG  
Sbjct: 361 FTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIYGHHDVPALEQQLVIKKETGFWRDFG 420

Query: 423 FGMTQCYSRDFINIGGFDLDIKGWGGED 450  
FGMTQCYSRDFINIG F + + GED  
Sbjct: 421 FGMTQCYSRDFINIGVFLVTLTDLMQGED 448

Score = 201 bits (510), Expect = 5e-50  
Identities = 90/97 (92%), Positives = 93/97 (95%)

Query: 436 IGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVVRGLFHLWHEKRCMDELTPEQYKCMQ 495  
+ GFDLDIKGWGGEDVHLYRKYLHSNLIV+RTPVRGLFHLWHEK CMDDELTPEQY+MCMQ  
Sbjct: 521 VRGFDLDIKGWGGEDVHLYRKYLHSNLIVIRTPVRGLFHLWHEKHCMDELTPEQYRMCMQ 580

Query: 496 SKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT 532  
SKAMNEASHGQLGMLVFRHEIEAHLRKQK K SSKKT  
Sbjct: 581 SKAMNEASHGQLGMLVFRHEIEAHLRKQKLKASSKKT 617

☐ >gi|47219910|emb|CAF97180.1| unnamed protein product [Tetraodon nigroviridis]  
Length = 607

Score = 720 bits (1858), Expect = 0.0  
Identities = 368/609 (60%), Positives = 447/609 (73%), Gaps = 83/609 (13%)

Query: 3 MVRRGLLAWISRVVLLVLLCCAISVLYMLACTP-KGDEEQLA--LPRA----- 48  
M+RRGLLAW+SRV +LVLLC ++S+LY++ C+P D L LPRA  
Sbjct: 1 MLRRGLLAWVSRVGGVLVLLCSSLSLLYLMTCSPPHSDNHPLGHVLPRAAPVRPSLGGTG 60

Query: 49 --NSPTGK-----EGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLR 94  
+ T K + YQ +LQE EEQHR ++SSLK+QIAQLKE LQERS+QL+  
Sbjct: 61 AGDVGTAARAAQNGAAPPQSYQVLLQEREEQHRLHISSLKQQAQLKEALQERSQQLK 120

Query: 95 NGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQ 154  
Q S GLG + P+ QADL +L SQ+ KAEV AG +L +EYA VPF+SFTLQ  
Sbjct: 121 G--VQESIKTGLG-EAHGPKSQQADLQDYLRSQLTKAEVTAGTRLPSEYAVVPFESFTLQ 177

Query: 155 KVYQLETGLTRHPPEEKPVKDKRDELVEAIESALETLN-----NPAENSPNHRPYT 205  
+VYQLETGLTRHPPEEKPVKDK+RDEL E +E+AL +LN PA+ +P + Y+  
Sbjct: 178 RVYQLETGLTRHPPEEKPVKDRRDELGEVLETALHSLNAPSAAQDDKTPAQKAPTSKVYS 237

Query: 206 ASDFIE-----GIYRTERDKGTYELTFKGDHKHEFKRLILFRPFSPIMKV 251  
SDF+E GI RTE+DKGT+YEL F+G+ +EF+RL+LFRPF P+MKV  
Sbjct: 238 PSDFVEDSSLSSVVHPGAFSGISRTEKDKGTYELIFRGEAANEFRRLVLFRRPFGPLMKV 297



Query: 252 KNEKLNMAANTLINIVIVPLAKRVDKFRQFMQNPREMCIEQDGRVHLTVVYFGKEEINEVKG 311  
 ++E+++ A+ IN++VPL++R DKF+QFM NFRE+C+ QDGRVHLTVVYFGKE+++EV+  
 Sbjct: 298 RSERVAASIPINIVVPLSRRSDKFKQFMHNFREVCVRQDGRVHLTVVYFGKEQMSEVRS 357

Query: 312 ILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTC 371  
 LENTS+ F+N+T +QL+ EFSRG+GLDVGAR W+G NVLLFFCDVDIYFT++FLN C  
 Sbjct: 358 TLENTSREVRFKNYTLLQLDEEFSRGRGLDVGARAWRGGNVLLFFCDVDIYFTADFLNAC 417

Query: 372 RLNTQPG-----KKVFYPVLFSQYNPGIYGHHDV 402  
 RLN QPG KKVFYPVLFSQYNP +IYG + V  
 Sbjct: 418 RLNAQPGETHHTHTLTCTRLVLLSLPGLMGSLSLPGKKVFYPVLFSQYNPALIYGSSEHV 477

Query: 403 PPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNL 462  
 PP+EQQLVIKK+TGFWRDFGFGMTCQYRSDFINIGGFD+DIKGWGGEDVHLYRKYLHSNL  
 Sbjct: 478 PPVEQQQLVIKKDTGFWRDFGFGMTCQYRSDFINIGGFDIDIKGWGGEDVHLYRKYLHSNL 537

Query: 463 IVVRTPVRLGFLHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLRK 522  
 +VVRTP RGLFHLWHEK C DEL P+QY+MCMQSKAMNEASHGQLGML FRHEIEAHLRK  
 Sbjct: 538 LVVRTPARGLFHLWHEKHCADELPDQYRMCMQSKAMNEASHGQLGMLFFRHEIEAHLRK 597

Query: 523 QKQKTSSKK 531  
 QKQ+ ++ K  
 Sbjct: 598 QKQQNANLK 606

☐ >gi|24429592|ref|NP\_061060.3| chondroitin beta1,4N-acetylgalactosaminyltransf  
 sapiens]  
 gi|20988438|gb|AAH30268.1| Chondroitin beta1,4 N-acetylgalactosaminyltransferase  
 sapiens]  
 gi|27922994|dbj|BAC55935.1| beta-1,4-N-acethylgalactosaminyltransferase [Homo sa  
 gi|27923015|dbj|BAC55936.1| chondroitin beta1,4 N-acetylgalactosaminyltransferase  
 sapiens]  
 Length = 542

Score = 665 bits (1717), Expect = 0.0

Identities = 316/512 (61%), Positives = 396/512 (77%), Gaps = 11/512 (2%)

Query: 29 LYMLACTPKGDEEQALPRANSPTGKEGYQAVLQEWEEQHRNVSSSLKRQIAQLKEELQE 88  
 +Y+L C P+ D GKE YQA+LQE EE ++ +SLKRQIAQLK+ELQE  
 Sbjct: 29 MYLLECAPQTDGNASLPGVVGENYGYKEYYQALLQEQQEHHYQTRATSLKRQIAQLKQELQE 88

Query: 89 RSEQLRNGQYQAS-DAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVP 147  
 SE++R+ Q + + A G+G +S E+ +DLL FLHSQ+DKAEV+ G KL +EY +P  
 Sbjct: 89 MSEKMRSIQERRNVGANGIGY-QSNKEQAPSDLLEFLHSQIDKAEVSIGAKLPSEYGVIP 147

Query: 148 FDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETNNPAENSPNHRP---- 203  
 F+SFTL KV+QLE GLTRHPEEKPVKDKRDELVE IE+ LE +NNP E+  
 Sbjct: 148 FESFTLMKVFQLEMGLTRHPEEKPVKDKRDELVEIEAGLEVINNPDDEDEQEDEEGPL 207

Query: 204 -----YTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLN 258  
 + +DF+EG YRTERDKGT YEL FK E++ + LFRPF P+MKVK+E +++  
 Sbjct: 208 GEKLIFNENDFVEGYRTERDKGTQYELFFKKADLTEYRHVTLFRPFGPLMKVKSEMIDI 267

Query: 259 ANT LINIVIVPLAKRVDKFRQFMQNPREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSK 318  
 ++IN+IVPLA+R + F QFMQNFR++CI QD ++HLTVVYFGKE +++VK ILE+ +  
 Sbjct: 268 TRSIINIIVPLAERTEAFVQFMQNFRDVCIHQDKKIHLTVVYFGKEGLSKVKSILESPTS 327

Query: 319 AANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPG 378  
 +NF N+T + LN EF+RG+GL+VGAR W VL+FFCDVDIYF++EFLN+CRLN +PG  
 Sbjct: 328 ESNFHNITLVSLNEEFNRGRGLNVGARAWDKGEVLMFFCDVDIYFSAEFLNSCRLNAEPG 387

Query: 379 KKVFPYVLFVSQYNPGIYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGG 438  
 KKVFPV+FS YNP I+Y + + PP+EQQLV KK++GFWRDFGFGMTCQYRSDF+ IGG  
 Sbjct: 388 KKVFPVVSFLYNPAIVYANQEVPPPEEQQLVHKKDSGFWRDFGFGMTCQYRSDFLTIGG 447

Query: 439 FDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVGRGLFHLWHEKRCMDELTPSEQYKCMQSKA 498  
 FD+++KGWGGEDVHLYRKYLH +LIV+RTPV GLFHLWHEKRC DELTPSEQY+MC+QSKA  
 Sbjct: 448 FDMEVKGWGGEDVHLYRKYLHGLDLIVIRTPVPGLFHLWHEKRCDELTPSEQYRMCIQSKA 507

Query: 499 MNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530  
 MNEASH LGMLVFR EIE HL KQ +T+S+  
 Sbjct: 508 MNEASHSHLGMLVFREEIETHLHKQAYRTNSE 539

>gi|31560032|ref|NP\_084441.3| chondroitin sulfate GalNAcT-2 [Mus musculus]  
 gi|26389329|dbj|BAC25717.1| unnamed protein product [Mus musculus]  
 Length = 542

Score = 659 bits (1701), Expect = 0.0  
 Identities = 315/514 (61%), Positives = 394/514 (76%), Gaps = 15/514 (2%)

Query: 29 LYMLACTPKGDEEQALPRANSPTGKEGYQAVLQEWEEQHRNVSSSLKRQIAQLKEELQE 88  
 +Y+L C P+ D GKE YQA+LQE EE ++ +SLKRQIAQLK+ELQ+  
 Sbjct: 29 MYLLECAPQTDGNASLPGVVRENYGKEYYQALLQEQQEHHYQTRATSLKRQIAQLKQELQD 88

Query: 89 RSEQLRNGQYQAS-DAAGLGLDRSPPEKTQA--DLLAFLHSQVDKAEVNAGVKLATEYAA 145  
 SE++R Q + A G+G P + QA DLL FLHSQ+D+AEV+ G KL +EY  
 Sbjct: 89 MSEKMRALQERKKLGANGVG---PGNREQAPSDLLEFLHSQIDRAEVSVAKLPSEYGV 145

Query: 146 VPFDSFTLQKVYQLETGLTRHPPEKPVKDKRDELVEAIESALETNNPAENSPNHRP-- 203  
 VPF+SFTL KV+QLE GLTRHPPEKPVKDKRDELVE IE+ +E +NNP E+  
 Sbjct: 146 VPFESFTLMKVQLEMGLTRHPPEKPVKDKRDELVEVIEAGVEVINNPDEDDAQEDEEG 205

Query: 204 -----YTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKL 256  
 + +DFIEG YRTERDKGT YEL FK E++ + LFRPF P+MKVKNE +  
 Sbjct: 206 PLGEKLIFNENDFIEGYRTERDKGTQYELFFKKADLMEYRHVTLFRPFGPLMKVKNELI 265

Query: 257 NMANTLINIVVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENT 316  
 ++ ++IN+IVPLA+R + F QFMQNF++CI QD R+HLTVVYFGKE +++VK ILE+  
 Sbjct: 266 DITRSVINIIVPLAERTEAFSQFMQNFQDVCIHQDKRIHLTVVYFGKEGLSKVKSILES 325

Query: 317 SKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQ 376  
 S ++F N+T + L+ EF+RG+GL+VGAR W VL+FFCDVDIYF++EFLN+CRLN +  
 Sbjct: 326 SSESDFHNYTLVSLDEEFNRGRGLNVGARAWDKGEVLMFFCDVDIYFSAEFLNSCRLNAE 385

Query: 377 PGKKVFYFVLFYQYNPGIIYGHDAVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINI 436  
 PGKKVFYFV+FS YNP I+Y + D PP+EQQLV KK++GFWRDFGFGMTCQY+SDF+++  
 Sbjct: 386 PGKKVFYFVVFSLYNPAIVYANQDVPVPPVEQQQLVHKKDSGFWRDFGFGMTCQYQSDFLSV 445

Query: 437 GGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVGRGLFHLWHEKRCMDELTPSEQYKCMQSKA 496  
 GGFDD+++KGWGGEDVHLYRKYLH +LIV+RTPV GLFHLWHEK C DELTPSEQY+MC+QS  
 Sbjct: 446 GGFDMVKGWGGEDVHLYRKYLHGLDLIVIRTPVPGLFHLWHEKHCDELTPSEQYRMCIQS 505

Query: 497 KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530  
 KAMNEASH LGM+VFR EIE HLRKQ +T+S+  
 Sbjct: 506 KAMNEASHSHLGMMVFREEIEMHLRKQAYRTNSE 539

>gi|26386533|dbj|BAB31761.2| unnamed protein product [Mus musculus]  
 Length = 542

Score = 657 bits (1696), Expect = 0.0  
 Identities = 314/514 (61%), Positives = 394/514 (76%), Gaps = 15/514 (2%)

Query: 29 LYMLACTPKGDEEQALPRANSPTGKEGYQAVLQEWEEQHRNVSSSLKRQIAQLKEELQE 88  
 +Y+L C P+ D GKE YQA+LQE EE ++ +SLKRQIAQLK+ELQ+  
 Sbjct: 29 MYLLECAPQTDGNASLPGVVRENYGKEYYQALLQEQQEHHYQTRATSLKRQIAQLKQELQD 88

Query: 89 RSEQLRNGQYQAS-DAAGLGLDRSPPEKTQA--DLLAFLHSQVDKAEVNAGVKLATEYAA 145  
 SE++R Q + A G+G P + QA DLL FLHSQ+D+AEV+ G KL +EY  
 Sbjct: 89 MSEKMRALQERKKLGANGVG---PGNREQAPSDLLEFLHSQIDRAEVSVAKLPSEYGV 145

Query: 146 VPFDSTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAENSPNHRP-- 203  
 VPF+SFTL KV+QLE GLTRHPEEKPVKDKRDELVE IE+ +E +NNP E+  
 Sbjct: 146 VPFEFTLMKVQFQLEMGLTRHPEEKPVKDKRDELVEIEAGVEVINNPDEDDAQEDEEG 205

Query: 204 -----YTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKL 256  
 + +DFIEG YRTERDKGT YEL FK E++ + LFRPF P+MKVKNE +  
 Sbjct: 206 PLGEKLIFNENDFIEGYRTERDKGTQYELFFKKADLMEYRHVTLFRPFGPLMKVKNELI 265

Query: 257 NMANTLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENT 316  
 ++ ++IN+IVPLA+R + F QFMQNF++CI QD R+HLTVVYFGKE +++VK ILE+  
 Sbjct: 266 DITRSVINIIVPLAERTEAFSQFMQNFQDVCIHQDKRIHLTVVYFGKEGLSKVKSILESV 325

Query: 317 SKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQ 376  
 S ++F N+T + L+ EF+RG+GL+VGAR W VL+FFCDVDIYF++EFLN+CRLN +  
 Sbjct: 326 SSESDFHNYTLVSLDEEFNRGRGLNVGARAWDKGEVLMFFCDVDIYFSAEFLNSCRLNAE 385

Query: 377 PGKKVFYFVLFQSYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINI 436  
 PGKKVFYFV+F+ YNP I+Y + D PP+EQQLV KK++GFWRDFGFGMTCQY+SDF+++  
 Sbjct: 386 PGKKVFYFVFNLYNPAIVYANQDVPPVEQQLVHKKDSGFWRDFGFGMTCQYQSDFLSV 445

Query: 437 GGFDDLKIGWGGEDVHLYRKYLHNSLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMQS 496  
 GGF+++KGWGGEDVHLYRKYLH +LIV+RTPV GLFHLWHEK C DELTPQY+MC+QS  
 Sbjct: 446 GGFDEMEVKGWGGEDVHLYRKYLHGDLLIVRTVPVGLFHLWHEKHCADELTPQYRMCIQS 505

Query: 497 KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSK 530  
 KAMNEASH LGM+VFR EIE HLRKQ +T+S+  
 Sbjct: 506 KAMNEASHSLGMMVFREEIEMHLRKQAYRTNSE 539

☐ >qi|47227595|emb|CAG09592.1|... unnamed protein product [Tetraodon nigroviridis]  
 Length = 496

Score = 577 bits (1487), Expect = e-163

Identities = 284/494 (57%), Positives = 370/494 (74%), Gaps = 28/494 (5%)

Query: 52 TGKEGYQAVLQEWEEQHRNYVSSLRQIAQLKEELQERSEQLRNGQYQASDAAGL--GLD 109  
 T +EGY A+LQE E+ HR Y++SL RQI QLKE L ER++QL++ +A L GL+  
 Sbjct: 3 TSREGYMALLQEREDSHRRYINSLTRQIQQLKEALLERTQQLQDSLEKAQTGGILPGGLE 62

Query: 110 RSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQK----- 155  
 TQ+DL FL SQ+D+AEVN+GVKL+ EY +P+D+FTLQ+  
 Sbjct: 63 SLRKTPTQSDLKEFLRSQLDRAEVNSGVKLSGEYEVIPYDTFTLQRWVTELKPKSPMWLH 122

Query: 156 -----VYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAEN---SPNHRPY 204  
 VYQLETGL+RHPEE+PVR+D+R EL A+E+AL LN P ++ + +  
 Sbjct: 123 REALSPRVYQLETGLSRHPEERPVRDRRAELTGAVETALHLLNGPEQHGDGAAGKHTH 182

Query: 205 TASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLNMAANTLIN 264  
 + +DF+EG+ RTERD+GT+YELTFK +L+LFRPF P++KV++E +++++ L+N  
 Sbjct: 183 SPADFVEGLTRTERDRGTVYELTFKDKGPRGLSQLVLFRPFGPLLKVRSESVDLSSVLVN 242

Query: 265 VIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRN 324  
 V+VPL+ R + FR+F+ NFR CI+QDGRVHLTVV+FG + + +VK +L+ TS+ FRN  
 Sbjct: 243 VVVPLSGRTEAFRRFIANFRACIQDGRVHLTVVHFGGDPVEQVKALLDQTSRETRFRN 302

Query: 325 FTFIQLNGEFSRGKGLDVGARFWKGS-NVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVY 383  
 FT IQLN FSRG+GL++GAR W+ S NVLLFFCDVD++FT++FL +CRLN PGKKV+Y  
 Sbjct: 303 FTLIQLNEVFSRGRGLEIGARAWRRSQNVLLFFCDVDVHFTADFLTSCRLNALPGKKVYY 362

Query: 384 PVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDLI 443  
 PVLFS YNP +IY +H P L+QQLVI+KE+GFWRDFGFGMTCQYRSDFINIGGF I  
 Sbjct: 363 PVLFSLYNPSVIYHNHHTHPPSLQQQLVIRKESGFWRDFGFGMTCQYRSDFINIGGFDRAI 422

Query: 444 KGWGGEDVHLYRKYLHNSLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMQSKAMNEAS 503  
 +GWG EDVHLYRKYLH L+VVR+P R LFHLWHEK C DEL P++Y+MCMQ+KA++EAS  
 Sbjct: 423 RGWGLEDVHLYRKYLHSLKLMVVRSPSRSLFHLWHEKVCADLPPDKYRMCMQTKAVSEAS 482

Query: 504 HGQLGMLVFRHEIE 517  
 HG+LG LVFR E  
 Sbjct: 483 HGRLGELVFRRRDE 496

☐ >gi|38174240|gb|AAH60772.1| ChGn protein [Homo sapiens]  
 Length = 297

Score = 557 bits (1436), Expect = e-157  
 Identities = 282/284 (99%), Positives = 283/284 (99%)

Query: 1 MMMVRRGLLAWISRVVLLVLLCCAI SVLYMLACTPKGDEEQLALPRANSPTGKEGYQAV 60  
 MMMVRRGLLAWISRVVLLVLLCCAI SVLYMLACTPKGDEEQLALPRANSPTGKEGYQAV  
 Sbjct: 1 MMMVRRGLLAWISRVVLLVLLCCAI SVLYMLACTPKGDEEQLALPRANSPTGKEGYQAV 60

Query: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120  
 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL  
 Sbjct: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 180  
 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL  
 Sbjct: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 180

Query: 181 VEAIESALETLLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240  
 VEAIESALETLLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI  
 Sbjct: 181 VEAIESALETLLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240

Query: 241 LFRPFSPIMKVKNEKLN MANTLINVIVPLAKRVDKFRQFMQNFR 284  
 LFRPF PIMKV+NEKLN MANTLINVIVPLAKRVDKFRQFMQNFR  
 Sbjct: 241 LFRPFGPIMKVENEKLN MANTLINVIVPLAKRVDKFRQFMQNFR 284

☐ >gi|26340498|dbj|BAC33912.1| unnamed protein product [Mus musculus]  
 Length = 300

Score = 532 bits (1370), Expect = e-150  
 Identities = 262/302 (86%), Positives = 279/302 (92%), Gaps = 4/302 (1%)

Query: 3 MVRRGLLAWISRVVLLVLLCCAI SVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ 62  
 MVRRGLL WISRVV+LLVLLCCAI SVLYMLACTPKGD+EQL LPRAN PTGK+GYQAVLQ  
 Sbjct: 1 MVRRGLLWISRVVILLVLLCCAI SVLYMLACTPKGDQEQLGLPRANGPTGKDGQAVLQ 60

Query: 63 EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGL-GLDRSPPEKTQADL 120  
 E EEQHRNYV+SLKRQIAQLK+ELQ RSEQ R+GQ QASDA L G DR P K QADL  
 Sbjct: 61 EREEQHRNYVNSLKRQIAQLKDELQARSEQFRSGQDQASDATSLRSGWDREP--KAQADL 118

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 180  
 LAFL QVDKAEV+AGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL  
 Sbjct: 119 LAFLRGQVDKAEVHAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 178

Query: 181 VEAIESALETLLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240  
 VEAIESALE+LN+P E+SP+ RPYTA+DFIEGIYRTERDKGTLYELTFKGDHKHEF+RL+  
 Sbjct: 179 VEAIESALESINSPVESSPHQRPYTAADFIIEGIYRTERDKGTLYELTFKGDHKHEFQRLV 238

Query: 241 LFRPFSPIMKVKNEKLN MANTLINVIVPLAKRVDKFRQFMQNFRFREMCIQDGRVHLTVVY 300  
 LFRPF PIMKVK EKLN+ANTLINVIVPLA+RVDKFR FMQNFRFREMCI+QDGRVHLTVVY  
 Sbjct: 239 LFRPFGPIMKVKKEKLN LANTLINVIVPLARRVDKFRHFMQNFRFREMCIQDGRVHLTVVY 298

Query: 301 FG 302  
 FG  
 Sbjct: 299 FG 300

☐ >gi|7023813|dbj|BAA92093.1| unnamed protein product [Homo sapiens]  
 Length = 275

Score = 523 bits (1347), Expect = e-147


Identities = 238/239 (99%), Positives = 239/239 (100%)

Query: 283 FREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDV 342  
 FREMCIEQDGRVHLTVVYFGKEEINEVKG+LENTSKAANFRNFTFIQLNGEFSRGKGLDV  
 Sbjct: 26 FREMCIEQDGRVHLTVVYFGKEEINEVKGVLENTSKAANFRNFTFIQLNGEFSRGKGLDV 85

Query: 343 GARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYGHHDV 402  
 GARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYGHHDV  
 Sbjct: 86 GARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYGHHDV 145

Query: 403 PPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNL 462  
 PPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNL  
 Sbjct: 146 PPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNL 205

Query: 463 IVVRTPVRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521  
 IVVRTPVRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR  
 Sbjct: 206 IVVRTPVRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 264

 >gi|20072996|gb|AAH26599.1| 4732435N03Rik protein [Mus musculus]  
 Length = 239


Score = 494 bits (1272), Expect = e-138  
 Identities = 224/228 (98%), Positives = 226/228 (99%)

Query: 294 VHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVL 353  
 VHLTVVYFGKEE+NEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVL  
 Sbjct: 1 VHLTVVYFGKEEMNEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVL 60

Query: 354 LFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYGHHDVPPLEQQQLVIKK 413  
 LFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPG+IYGHHDVPPLEQQQLVIKK  
 Sbjct: 61 LFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGVIYGHHDVPPLEQQQLVIKK 120

Query: 414 ETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLF 473  
 ETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLF  
 Sbjct: 121 ETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLF 180

Query: 474 HLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521  
 HLWHEK CDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR  
 Sbjct: 181 HLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 228

 >gi|34858369|ref|XP\_232316.2| similar to chondroitin betal,4 N-acetylgalactosa  
 [Rattus norvegicus]  
 Length = 462

Score = 486 bits (1251), Expect = e-136  
 Identities = 214/317 (67%), Positives = 266/317 (83%)

Query: 214 YRTERDKGTYELTFKGDHKEFEKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRV 273  
 YRTERDKGT YEL FK E++ + LFRPF P+MKVK+E +++ ++IN+IVPLA+R  
 Sbjct: 143 YRTERDKGTHYELFFKADLMERYHVTLFRPFGPLMKVKSELIDITRSVINIIVPLAERT 202

Query: 274 DKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGE 333  
 + F QFMQNF++CI QD R+HLTVVYFGKE ++ VK ILE+ S +NF N+T + LN E  
 Sbjct: 203 EAFSQFMQNFQDVCIHQDKRIHLTVVYFGKEGLSTVKSILESVSSESNFHNYTLVSLNEE 262

Query: 334 FSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPG 393  
 F+RG+GL+VGAR W VL+FFCDVDIYF++EFLN+CRLN +PGKKVFYPV+FS YNP  
 Sbjct: 263 FNRGRGLNVGARTWDKGEVLMFFCDVDIYFSAEFLNSCRLNAEPGKKVFYPVVFSLYNPA 322

Query: 394 IYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHL 453  
 I+Y + + PP+EQQLV KK++GFWRDFGFGMTCQY+SDF+++GGFD+++KGWGGEDVHL  
 Sbjct: 323 IVYANQEVPPPVEQQQLVHKKDSGFWRDFGFGMTCQYQSDFLSVGGFDMEVKGWGGEDVHL 382

Query: 454 YRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFR 513  
 YRKYLH +LIV+RTPV GLFHLWHEK C DELTPQY+MC+QSKAMNEASH LGM+VFR

Sbjct: 383 YRKYLHGDIVIRTPVPGFLHLWHEKHCADLTPEQYRMCIQSKAMNEASHSHLGMMVFR 442

Query: 514 HEIEAHLRKQKQKTSSK 530

EIE HLRKQ +T+S+

Sbjct: 443 EEIEMHLRKQAYRTNSE 459

Score = 99.8 bits (247), Expect = 2e-19

Identities = 63/144 (43%), Positives = 87/144 (60%), Gaps = 4/144 (2%)

Query: 3 MVRRG--LLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAV 60

M RRG L + ++V L LL + +Y+L C P+ D GKE YQA+

Sbjct: 1 MSRRGPILHSRTQWLLVGLALLFSLVLFMYLLECAPQTDGNASLPGVVRENYGKEYYQAL 60

Query: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQAS-DAAGLGLDRSPPEKTQAD 119

LQE EE ++ +SLKRQIAQLK+ELQ+ SE++R Q + A G+G + E+T +D

Sbjct: 61 LQEQEEHYQTRATSLKRQIAQLKQELQDMSEKMRALQERKKLGANGIGY-QGNREQTPSD 119

Query: 120 LLAFLLHSQVDKAEVNAGVKLATEY 143

LL FLHSQ+D+AEV+ G KL + Y

Sbjct: 120 LLEFLHSQIDRAEVSIGAKLPSYY 143

☐ >gi|47216537|emb|CAG04715.1| unnamed protein product [Tetraodon nigroviridis]  
Length = 522

Score = 485 bits (1248), Expect = e-135

Identities = 235/413 (56%), Positives = 298/413 (72%), Gaps = 8/413 (1%)

Query: 34 CTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQERSEQL 93

CTP D + A GKE YQA+LQE EE+H N +SLKRQIAQLK+ELQE S++L

Sbjct: 34 CTPPADISLVLPGLAGENNGKEYYQALLQEQEERHLNRATSLKRQIAQLKQELQEMSDKL 93

Query: 94 RNGQYQASDAAGLGLDRSPPEKTQADLLAFLLHSQVDKAEVNAGVKLATEYAAVPFDSFTL 153

+ Q + A GL + ++ DLL +LHSQ+DKAEVN G + +EYA +PF+SFT

Sbjct: 94 KLLQDKKEPPAVQGLAETK-DQEPGDLDDLHSLQIDKAEVNTGARFPSEYALIPFESFTS 152

Query: 154 QKVYQLETGLTRHPPEEKPVRRDKRDELVEAIESALETNNP-----AENSPNHR-PYTA 206

KVYQLE GLTRHPPEEKPVRR+D+RDELVE +E+AL+ +NNP E+ P R YT

Sbjct: 153 SKVYQLEMGLTRHPPEEKPVRRDRRDELVEVVEAALDIINNPDDEEDGVEEDVPMQRQTYTE 212

Query: 207 SDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVI 266

F EG+YRTERDKGTLYEL F + F+ + LFRPF P+MKV++ + + +IN+I

Sbjct: 213 VHFTEGLYRTERDKGTLYELFFAKEDSSSRHVTLFRPFGPLMKVRSTSVETSGAIINII 272

Query: 267 VPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFT 326

VPL+ RV+ F QF+ NFRE+CI D RVHLTVVYFG+E + EVK LE S+ +F N+T

Sbjct: 273 VPLSGRVEAFSQFLHNFREVCILHDDRVLTVVYFGQEGLEVKSSLEKVSREESFSNYT 332

Query: 327 FIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVL 386

I ++ EFSRG+GLD+GA WK +VL+FFCDVDI+F+ EFLNTCRL+ P K+VFYPV+

Sbjct: 333 LIPVDEEFSRGRGLDIGAHAWKRGDVLMMFFCDVDIHFSLEFLNTCRLHAAPNKRVPV 392

Query: 387 FSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGF 439

FS YNP I+YG+ + PP+E QL+ KK+ GFWRDFGFGMTCQYRSDF+NI F

Sbjct: 393 FSLYNPAIVYGNLELAPPIELQLIHKKDAGFWRDFGFGMTCQYRSDFLNIAF 445

☐ >gi|31198419|ref|XP\_308157.1| ENSANGP00000021559 [Anopheles gambiae]  
gi|21292063|gb|EAA04208.1| ENSANGP00000021559 [Anopheles gambiae str. PEST]  
Length = 648

Score = 382 bits (982), Expect = e-105

Identities = 222/547 (40%), Positives = 310/547 (56%), Gaps = 68/547 (12%)

Query: 47 RANSPTGKEGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQA----- 100

+A++ + GY +LQ+ EE++ V+ L +I LK ++ QL+NG A

Sbjct: 81 QADAEQQQNGYMQMLQQREEENLKEVAKLTAEIKALKLQIL---QLKNGLTNAGMGVMQ 136  
 Query: 101 ----SDAAGLGLDRSP-----PEKTQA--DLLAFLHSQVDKAEVNAGVKLATEYAAVPFD 149  
           A L D S       P+ +Q D AF+ QV AE+ G+ L EY +PF+  
 Sbjct: 137 PNVVEAAVSLSDSSAIVANAPQTSQMLHDCATFIRRQVGSAEILHGLPLNNEYELIPFN 196  
 Query: 150 SFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAENSPNHRPYTASDF 209  
           FT +VY +E GL +   EKP+ KR +++ A+ ALETLN A +S   YT DF  
 Sbjct: 197 HFTFSRVYPIELGLGKRVVEKPIGY-KRKDILSALNKALETLNRNASSSAQR--YTLDDF 253  
 Query: 210 IEGIYRTERDKGTLYELTFKGDHK-----HEFKRLILFRPFSPIMKVKN 253  
           IEGIYR E GT YEL F+                           H +LI+ RPF+ + V+  
 Sbjct: 254 IEGIYRNEPTTGTQYELYFRTKESANRSQQQQQIAQHSHSGTTKLIVMRPFASLQTVQL 313  
 Query: 254 EKLN--MANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKG 311  
           E +            +I +I+PL+ R F+ FM+ + ++ ++ D RVHLTVVYFG+E + E +  
 Sbjct: 314 EAYSKHQEKEIIYIILPLSGRTSTFQSFMEKYVKIALKHDKRVHLTVVYFGEEGLAEART 373  
 Query: 312 ILENT---SKAANFRNFTFIQLNGEFSRGKGLDVGAR-FW----KGSNVLLFFCDVDI 361  
           I+            + A N + LN FSR K L VGA W K +++LLF CDVDI  
 Sbjct: 374 IMSRVIGMKNSGATNSNLKLLALNETFSRAKALRVGAENVWSSQADKNNDILLFMCDDVI 433  
 Query: 362 YFTSEFLNTCRLNTQPGKKVFYPVLFQYNGPIIYG-HHDAVPPLEQQQLVIKKETGFWRD 420  
           F+++FL+ CR NT+P KKV+YPV+FS YNP ++Y VPP QLVI K++GFWRD  
 Sbjct: 434 VFSAKFLDRCRWNTKPNKKVYYPVVFSLYNPHVVYTLQGKDVPPETDQLVISKDSGFWRD 493  
 Query: 421 FGFGMTCQYRSDFINIGGFDLIDKGGWGEDVHLYRKYLSNLIVVTPVRGLFHLWHEKR 480  
           FG+GMTCQYRSDF+ + GFD +I GGGWGEDV LYRKY+ S++ V+R G+FH+WH K  
 Sbjct: 494 FGYGMTCQYRSDFLRVGRGFDEEIIIGWGGEDVMVLYRKYVRSIKVIRATDPGVFHIWHPKV 553  
 Query: 481 CM-----DELTPEQYKMCQSKAMNEASHGQLGMLVFRHEIEAHL-----RKQKQ 525  
           C                   LT +QY+ C++S+A+NEASH QLG L FR +I A+ K Q  
 Sbjct: 554 CTGPVMSVTSNQRLTLDQYRACIRSRALNEASHAQLGFLAFRDDIAANEYILAQGAALNQ 613  
 Query: 526 KTSSKKT 532  
           ++S+ KT  
 Sbjct: 614 ESSTTKT 620

☐ >gi|34365000|emb|CA546036.1|      hypothetical protein [Homo sapiens]  
                                   Length = 216

Score = 361 bits (927), Expect = 2e-98  
 Identities = 154/211 (72%), Positives = 183/211 (86%)

Query: 320 ANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379  
           +NF N+T + LN EF+RG+GL+VGAR W VL+FFCDVDIYF++EFLN+CRLN +PGK  
 Sbjct: 3 SNFHNHYTLVSLNEEFNRRGRGLNVGARAWDKGEVLMFFCDVDIYFSAEFLNSCRLNAEPGK 62  
 Query: 380 KVFYPVLFQYNGPIIYGHDAVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGF 439  
           KVFYPV+FS YNP I+Y + + PP+EQQLV KK++GFWRDFGFGMTCQYRSDF+ IGGF  
 Sbjct: 63 KVFYPVVFSLYNPAIVYANQEVPPPVEQQLVHKKDSGFWRDFGFGMTCQYRSDFLTIGGF 122  
 Query: 440 DLDIKGGWGEDVHLYRKYLSNLIVVTPVRGLFHLWHEKRCMDLTPEQYKMCQSKAM 499  
           D+++KGWGGEDVHLYRKYLSH +LIV+RTPV GLFHLWHEKRC DELTPEQY+MC+QSKAM  
 Sbjct: 123 DMEVKGWGGEDVHLYRKYLSHGLDILVIRTPVSGLFHLWHEKRCADLTPEQYRMCIQSKAM 182  
 Query: 500 NEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530  
           NEASH LGMLVFR EIE HL KQ +T+S+  
 Sbjct: 183 NEASHSHLGMLVFREIEIETHLHKQAYRTNSE 213

☐ >gi|24652379|ref|NP\_610567.1|      CG12913-PA [Drosophila melanogaster]  
☐ gi|7303771|gb|AAF58819.1|      CG12913-PA [Drosophila melanogaster]  
                                   Length = 540

Score = 351 bits (901), Expect = 2e-95

Identities = 208/519 (40%), Positives = 293/519 (56%), Gaps = 59/519 (11%)

Query: 39 DEEQALPRANSPTGKEGYQAVLQEWEE---EQHRNYVSSLKRQIAQLKEELQERSEQLRN 95  
 DE +AN+P+ G+ L E E E+ + V +L+ QI L+ + + N  
 Sbjct: 34 DELTTRETQANNPSESSGFSYTLSEAEIERLKQEV LALRTQILFLQN--NRSTAKPSN 91

Query: 96 GQYQASDAAGLGLDRSPPEKT---QADLLAFLHSQVDKAEVNAGVKLATEYAAVPPFDSFT 152  
 G Q + PP D +++ QV AE+ G+ L EY +P++ FT  
 Sbjct: 92 GSLQLQETTA-----GPPTAPLGHYDCSSYIRKQVGAAEILHGLPLNNEYELIPYNHFT 146

Query: 153 LQKVYQLETGLTRHPEEKPVRRKDKRDELVEAIESALETINNPAENSPNHRP----- 203  
 +VY ++ GL + EKP+ +RD L+EA+ ALE+LN +S R  
 Sbjct: 147 FTRVYPIDLGLGKRVEKPIGYRRRD-LIEAVNKALESLNR--NHSARIRAKGAGSAAAY 203

Query: 204 -----YTASDFIEGIYRTERDKGTLYELTFKGDHKHE---FKRLILFRPFSPIMKVKNE 254  
 YT DFIEGIYR E GT YEL F+ KH+ +R ++ RPF+P+ V+  
 Sbjct: 204 ASDVIKYTLDDFIEGIYRNEPTTGTQYELYFQ-SVKHQASPVRRALVMRPFAPLQTVQLS 262


Query: 255 KLNMA-----NTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGK 303  
 +L+ + +I+VI+PLA R+ FR F+Q F ++ +D R+ L VVYFG  
 Sbjct: 263 ELSSSVDNSGAPPSSHSPPIIHVILPLAGRLHSFRGFLQMFAL---EDRRLELIVVYFG- 318

Query: 304 EEINEVGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGS--NVLLFFCDVDI 361  
 G+ + S A + F+ LN FSR K L +GA + + +VLLF CDVDI  
 Sbjct: 319 -----TSGLEQARSLAGRSQRTQFLALNETFSRAKALRLGAEHIQPAEEDVLLFMCDVDI 373

Query: 362 YFTSEFLNTCRLNTQPGKKVFYPVLFQSYNPGIYIG-HHDAVPPLEQQQLVIKKETGFWRD 420  
 FT++FL CR N PGKKV+YPV+FS YNP ++Y +P E+QLVI ++TGFWRD  
 Sbjct: 374 MFTTKFLERCWNAAPGKKVYYPVVFSLYNPHVVYSLQGKPLPSEEEQLVISRDTGFWRD 433

Query: 421 FGFGMTCQYRSDFINIGGFDLD-IKGWGGEDVHLYRKYLSNLIVVRTPVRLGFHLWHEK 479  
 FG+GMTQCQYRS+F+ + GFD + I GWGGEDV LYRKY+ S + ++R G+FH WH K  
 Sbjct: 434 FGYGMTQCQYRSNFLKVRGFDEEEIVGWGGEDVMLYRKYVRSKIKIIRATDPGIFHRWHTK 493

Query: 480 RCMDELTPQYKMCQMCKAMNEASHGQLGMLVFRHEIEA 518  
 C LT +QY+ C++S+A+NEASH QLG L FR +I A  
 Sbjct: 494 ICSSSLTADQYRACIRSRALNEASHAQLGFLAFRDDIAA 532


 >gi|11360289|pir||T46919 hypothetical protein DKFZp762L037.1 - human (fragment)  
 gi|7018526|emb|CAE75673.1| hypothetical protein [Homo sapiens]  
 Length = 152

Score = 317 bits (812), Expect = 5e-85  
 Identities = 141/141 (100%), Positives = 141/141 (100%)

Query: 381 VFYPVLFQSYNPGIYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFD 440  
 VFYPVLFQSYNPGIYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFD  
 Sbjct: 1 VFYPVLFQSYNPGIYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFD 60

Query: 441 LDIKGWGGEDVHLYRKYLSNLIVVRTPVRLGFHLWHEKRCMDELTPQYKMCQMCKAMN 500  
 LDIKGWGGEDVHLYRKYLSNLIVVRTPVRLGFHLWHEKRCMDELTPQYKMCQMCKAMN  
 Sbjct: 61 LDIKGWGGEDVHLYRKYLSNLIVVRTPVRLGFHLWHEKRCMDELTPQYKMCQMCKAMN 120

Query: 501 EASHGQLGMLVFRHEIEAHLR 521  
 EASHGQLGMLVFRHEIEAHLR  
 Sbjct: 121 EASHGQLGMLVFRHEIEAHLR 141

 >gi|18677088|dbj|EAB35092.1| unnamed protein product [Homo sapiens]  
 Length = 180

Score = 317 bits (811), Expect = 5e-85  
 Identities = 134/177 (75%), Positives = 158/177 (89%)

Query: 354 LFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFQSYNPGIYGHHDVPPLEQQQLVIKK 413  
 +FFCDVDIYF++EFLN+CRLN +PGKKVFYPV+FS YNP I+Y + + PP+EQQLV KK




Sbjct: 1 MFFCDVDIYFSAEFLNSCRLNAEPGKKVFYPVVSFLYNPAIVYANQEVPPPVEQQLVHKK 60

Query: 414 ETGFWRDFGFGMTCQYRSDFINIGGFDLIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGF 473  
 ++GFWRDFGFGMTCQ+RSDF+ IGGFD+++KGWGGEDVHLYRKYLH +LIV+RTPV GLF

Sbjct: 61 DSGFWRDFGFGMTCQHRSDFLTIGGFDMEVKGWGGEDVHLYRKYLHGDIVIRTPVPGLF 120

Query: 474 HLWHEKRCMDELTPPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530  
 HLWHEKRC DELTPPEQY+MC+QSKAMNEASH LGMLVFR EIE HL KQ +T+S+

Sbjct: 121 HLWHEKRCADELTPEQYRMCIQSKAMNEASHSHLGMLVFREEIETHLHKQAYRTNSE 177

 >gi|34365310|emb|CAE45982.1| hypothetical protein [Homo sapiens]  
 Length = 333

Score = 314 bits (805), Expect = 3e-84  
 Identities = 163/303 (53%), Positives = 216/303 (71%), Gaps = 11/303 (3%)

Query: 29 LYMLACTPKGDEEQALPRANSPTGKEGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQE 88  
 +Y+L C P+ D GKE YQA+LQE EE ++ +SLKRQIAQLK+ELQE

Sbjct: 29 MYLLECAPQTDGNASLPGVVGENYGKEYYQALLQEQQEHHYQTRATSLKRQIAQLKQELQE 88

Query: 89 RSEQLRNGQYQAS-DAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVP 147  
 SE++R+ Q + + A G+G +S E+ +DLL FLHSQ+DKAEV+ G KL +EY +P

Sbjct: 89 MSEKMRSLQERRNVGANGIGY-QSNKEQAPSDDLLEFLHSQIDKAEVSIGAKLPSEYGVIP 147

Query: 148 FDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAENSPNHRP---- 203  
 F+SFTL KV+QLE GLTRHPEEKPVKDKRDELVE IE+ LE +NNP E+

Sbjct: 148 FESFTLMKVFQLEMGLTRHPEEKPVKDKRDELVEIEAGLEVINNPDDEDEQEDEEGPL 207

Query: 204 -----YTASDFIEGIYRTERDKGTYELTFKGDHKEFKRLILFRPFSPIMKVKNELNM 258  
 + +DF+EG YRTERDKGT YEL FK E++ + LFRPF P+MKVK+E +++

Sbjct: 208 GEKLIFNENDFVEGYRTERDKGTQYELFFKKADLTEYRHVTLFRPFGPLMKVKSEMDI 267

Query: 259 ANTILINVIVPLAKRVDKFRQFMQNFRMCIEQDGRVHLTVVYFGKEEINEVKGILENTSK 318  
 ++IN+IVPLA+R + F QFMQNFR++CI QD ++HLTVVYFGKE +++VK ILE+ ++

Sbjct: 268 TRSIINIIVPLAERTEAFVQFMQNFRDVCIHQDKKIHLTVVYFGKEGLSKVKSILESVTR 327

Query: 319 AAN 321  
 A+

Sbjct: 328 LAS 330

 >gi|37805317|gb|AAH60169.1| Galnact2 protein [Mus musculus]  
 Length = 293

Score = 264 bits (675), Expect = 4e-69  
 Identities = 144/268 (53%), Positives = 182/268 (67%), Gaps = 15/268 (5%)

Query: 29 LYMLACTPKGDEEQALPRANSPTGKEGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQE 88  
 +Y+L C P+ D GKE YQA+LQE EE ++ +SLKRQIAQLK+ELQ+

Sbjct: 29 MYLLECAPQTDGNASLPGVVRENYGKEYYQALLQEQQEHHYQTRATSLKRQIAQLKQELQD 88

Query: 89 RSEQLRNGQYQAS-DAAGLGLDRSPPEKTQA--DLLAFLHSQVDKAEVNAGVKLATEYAA 145  
 SE++R Q + A G+G P + QA DLL FLHSQ+D+AEV+ G KL +EY

Sbjct: 89 MSEKMRALQERKKLGANGVGY---PGNREQAPSDLLLEFLHSQIDRAEVSIGAKLPSEYGV 145

Query: 146 VPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAENSPNHRP-- 203  
 VPF+SFTL KV+QLE GLTRHPEEKPVKDKRDELVE IE+ +E +NNP E+


Sbjct: 146 VPFESFTLMKVFQLEMGLTRHPEEKPVKDKRDELVEIEAGVEVINNPDEDDAQEDEEG 205

Query: 204 -----YTASDFIEGIYRTERDKGTYELTFKGDHKEFKRLILFRPFSPIMKVKNEL 256  
 + +DFIEG YRTERDKGT YEL FK E++ + LFRPF P+MKVKNE +

Sbjct: 206 PLGEKLIFNENDFIEGYRTERDKGTQYELFFKKADLMEYRHVTLFRPFGPLMKVKNELI 265

Query: 257 NMANTLINVIVPLAKRVDKFRQFMQNFR 284  
 ++ ++IN+IVPLA+R + F QFMQNFR

Sbjct: 266 DITRSVINIIVPLAERTEAFSQFMQNFR 293

 >gi|47201472|emb|CAF87906.1| unnamed protein product [Tetraodon nigroviridis]  
Length = 245

Score = 221 bits (563), Expect = 3e-56

Identities = 127/309 (41%), Positives = 167/309 (54%), Gaps = 71/309 (22%)

Query: 178 DELVEAIESALETNNP-----AENSPNHR-PYTASDFIEGIYRTERDKGTLYELTFKG 230  
DELVE +E+AL+ +NNP E+ P R YT F EG+YRTERDKGTLYEL F  
Sbjct: 1 DELVEVVEAALDIINNPDEEDGVEEDVPMQRQTYTEVHFTEGLYRTERDKGTLYELFFAK 60


Query: 231 DHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVDKFRQFMQNFREMCIEQ 290  
+ F+ + LFRPF P+MKV++ + + +IN+IVPL+ RV+ F QF+ NFRE+CI  
Sbjct: 61 EDSSSFHVTFLFRPFGLMKVRSVETSGAIINIIVPLSGRVEAFSQFLHNFREVCILH 120

Query: 291 DGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGS 350  
D RVHLTVVYFG+E + EVK LE S++ + ++ A FW+  
Sbjct: 121 DRRVHLTVVYFGQEGLEVKSSLEKVSRSIHKD-----AGFWRD- 160

Query: 351 NVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIYGHHDVAPPLEQQLV 410  
F + + S+FLN + + S +N +A+PPL  
Sbjct: 161 ----FGFGMTCQYRSDFLNIGKRSRG-----LSLFNAEFTENGCEAIPPLA---- 202

Query: 411 IKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNLIVV RTPVR 470  
GGFDL++KGWG EDVHLYRKYL S+LIV+RTPV  
Sbjct: 203 -----GGFDLEVKGWGEDVHLYRKYLRSDLIVIRTPVS 236

Query: 471 GLFHLWHEK 479  
LFHLWHEK  
Sbjct: 237 SLFHLWHEK 245

 >gi|37573674|dbj|BAC98832.1| chondroitin sulfate synthase [Homo sapiens]  
Length = 882

Score = 207 bits (527), Expect = 5e-52

Identities = 113/275 (41%), Positives = 160/275 (58%), Gaps = 21/275 (7%)


Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKE-----EINEVKGILEN 315  
++++VPL R D F +FM+NF MC+ V L ++ F ++ I +KG  
Sbjct: 621 VHILVPLIGRYDIFLRFMENFENMCLIPKQNVKLVIILFSRDSGQDSSKHIELIKGYQNK 680

Query: 316 TSKAANFRNFTFIQLNGEFSRGKGLDVG-ARFWKGSNVLLFFCDVDIYFTSEFLNTCRLN 374  
KA T I + GEFSRG GL++ A+F ++ LL FCDVD+ F +FL CR N  
Sbjct: 681 YPKA----EMTLIPMKGEFSRGLGLEMASAQF--DNDTLLLFCDVDLIFREDFLQRCRDN 734

Query: 375 TQPGKKVFYPVLFSQYNPGIYGHHDVAPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI 434  
T G++V+YP++FSQY+P + G + PP + + K+TGFWRD+G+G+TC Y+SD +  
Sbjct: 735 TIQQQQVYPIIFSQYDPKVTNGGN--PPTDDYFIFSKKTGFWRDYGYGITCIYKSDL 791

Query: 435 NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVV RTPVRGLFHLWHEKRCMDELTPQYKMCM 494  
GGFD I+GWG EDV LY K + S L R+ G+ H++H C L P+QYKMC+  
Sbjct: 792 GAGGFDTSIQGWGLEDVDLYNKVILSGLRPFERSQEVGVVHIFHPVHCDPNLDPKQYKMCL 851

Query: 495 QSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSS 529  
SKA AS QL L +E HL + +T S  
Sbjct: 852 GSKASTFASTMQLAEL---WLEKHLGVRYNRTLS 882

 >gi|42657273|ref|XP\_373440.2| chondroitin sulfate synthase 3 [Homo sapiens]  
Length = 882

Score = 207 bits (527), Expect = 5e-52

Identities = 113/275 (41%), Positives = 160/275 (58%), Gaps = 21/275 (7%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKE-----EINEVKGILEN 315  
++++VPL R D F +FM+NF MC+ V L ++ F ++ I +KG

Sbjct: 621 VHILVPLIGRYDIFLRFMENFENMCLIPKQNVKLVIILFSRDSGQDSSKHIELIKGYQNK 680

Query: 316 TSKAANFRNFTFIQLNGEFSRGKGLDVG-ARFWKGSNVLLFFCDVDIYFTSEFLNTCRLN 374  
 KA T I + GEFSRG GL++ A+F ++ LL FCDVD+ F +FL CR N

Sbjct: 681 YPKA----EMTLIPMKGEFSRGLGLEMASAQF--DNDTLLLFCDVDLIFREDFLQRCRDN 734

Query: 375 TQPGKKVFYFVPLFSQYNPGIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFI 434  
 T G++V+YP++FSQY+P + G + PP + + K+TGFWRD+G+G+TC Y+SD +

Sbjct: 735 TIQQQQVYYPPIIFSQYDPKVTNNGN--PPTDDYFIFSKKTGFWRDYGYGITCIYKSDLL 791

Query: 435 NIGGFDDLIDKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCM 494  
 GGFD I+GWG EDV LY K + S L R+ G+ H++H C L P+QYKMC+

Sbjct: 792 GAGGFDTSIQGWGLEVDLYNKVILSGLRPFRSQEVGVVHIFHPVHCDPNLDPKQYKMCL 851

Query: 495 QSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSS 529  
 SKA AS QL L +E HL + +T S

Sbjct: 852 GSKASTFASTMQLAEL----WLEKHLGVRYNRTLS 882

☐ >gi|41529141|emb|CAE17326.1| chodroitin synthase 2 [Homo sapiens]  
 Length = 882

Score = 207 bits (526), Expect = 6e-52  
 Identities = 113/275 (41%), Positives = 160/275 (58%), Gaps = 21/275 (7%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKE-----EINEVKGILEN 315  
 ++++VPL R D F +FM+NF MC+ V L ++ F ++ I +KG

Sbjct: 621 VHILVPLIGRYDIFLRFMENFENMCLIPKQNVKLVIILFSRDSGQDSSKHIELIKGYQNK 680

Query: 316 TSKAANFRNFTFIQLNGEFSRGKGLDVG-ARFWKGSNVLLFFCDVDIYFTSEFLNTCRLN 374  
 KA T I + GEFSRG GL++ A+F ++ LL FCDVD+ F +FL CR N

Sbjct: 681 YPKA----EMTLIPMKGEFSRGLGLEMASAQF--DNDTLLLFCDVDLIFREDFLQRCRDN 734

Query: 375 TQPGKKVFYFVPLFSQYNPGIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFI 434  
 T G++V+YP++FSQY+P + G + PP + + K+TGFWRD+G+G+TC Y+SD +

Sbjct: 735 TIQQQQVYYPPIIFSQYDPKVTNNGN--PPTDDYFIFSKKTGFWRDYGYGITCIYKSDLL 791

Query: 435 NIGGFDDLIDKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCM 494  
 GGFD I+GWG EDV LY K + S L R+ G+ H++H C L P+QYKMC+

Sbjct: 792 GAGGFDTSIQGWGLEVDLYNKVILSGLRPFRSQEVGVVHIFHPVHCDPNLDPKQYKMCL 851

Query: 495 QSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSS 529  
 SKA AS QL L +E HL + +T S

Sbjct: 852 GSKANTFASTMQLAEL----WLEKHLGVRYNRTLS 882

☐ >gi|27681143|ref|XP\_225912.1| similar to carbohydrate (chondroitin) synthase 2  
 norvegicus]  
 Length = 561

Score = 206 bits (524), Expect = 1e-51  
 Identities = 112/271 (41%), Positives = 160/271 (59%), Gaps = 13/271 (4%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYF---GKEEINEVKGILENTSK 318  
 ++++VPL R D F +FM+NF CI V L ++ F G+E I ++ I E ++

Sbjct: 300 VHILVPLVGRYDIFLRFMENFESTCIIPKQNVKLVIILFSRDSGQESIKHIELIQEYQNR 359

Query: 319 AANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPG 378  
 + T I + GEFSRG GL++G+ + ++ LL FCDVD+ F +FL CR NT G

Sbjct: 360 YPS-AEMTLIPMKGEFSRGLGLEMGSSQFD-NDTLLLFCDVDLIFRGDFLQRCRDNTVQG 417

Query: 379 KKVYFVPLFSQYNPGIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGG 438  
 ++V+YP++FSQY+P + P E V KETGFWRD+G+G+TC Y+SD + GG

Sbjct: 418 QQVYYPPIIFSQYDPKVTNMGNS---PTEGDFVFSKETGFWRDYGYGITCIYKSDLLGAGG 474

Query: 439 FDLIDKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMQSKA 498  
 FD I+GWG EDV LY K + S L R+ G+ H++H C L P+QYKMC+ SKA

Sbjct: 475 FDTSIQGWGLEDVDLYNKVIQSGLRPFERSQEVGVVHIFHPVHCDPNLDPKQYKMCLGSKA 534

Query: 499 MNEASHGQLGMLVFRHEIEAHLRKQKQKTSS 529

AS +L L +E HL + +T S

Sbjct: 535 STFASTMKLAEL---WLEKHLGVRDNRTLS 561

☐ >gi|28411190|emb|CAD43233.1| chondroitin synthase 2 [Homo sapiens]  
Length = 573

Score = 206 bits (523), Expect = 1e-51

Identities = 113/275 (41%), Positives = 160/275 (58%), Gaps = 21/275 (7%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKE-----EINEVKGILEN 315

++++VPL R D F +FM+NF MC+ V L ++ F ++ I +KG

Sbjct: 312 VHILVPLIGRYDIFLRFMENFENMCLIPKQNVKLVIILFSRDSGQDSSKHIELIKGYQNK 371

Query: 316 TSKAANFRNFTFIQLNGEFSRGKGLDVG-ARFWKGSNVLLFFCDVDIYFTSEFLNTRCLN 374

KA T I + GEFSRG GL++ A+F ++ LL FCDVD+ F +FL CR N

Sbjct: 372 YPKA---EMTLIPMKGEFSRGLGLEMASAQF--DNDTLLLFCDVDLIFREDFLQRCRDN 425

Query: 375 TQPGKKVFYPVLFSSQYNPGIIGHHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI 434

T G++V+YP++FSQY+P + G + PP + + K+TGFWRD+G+G+TC Y+SD +

Sbjct: 426 TIQGGQVYPIIFSQYDPKVTNGGN--PPTDDYFIFSKKTGFWRDYGIGITCIYKSDLL 482

Query: 435 NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVTRTPVRGLFHLWHEKRCMDELTPQYKMCM 494

GGFD I+GWG EDV LY K + S L R+ G+ H++H C L P+QYKMC+

Sbjct: 483 GAGGFDTSIQGWGLEDVDLYNKVILSGLRPFERSQEVGVVHIFHPVHCDPNLDPKQYKMCL 542

Query: 495 QSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSS 529

SKA AS QL L +E HL + +T S

Sbjct: 543 GSKANTFASTMQLAEL---WLEKHLGVRYNRTLS 573

☐ >gi|7959793|gb|AAF71068.1| PRO0082 [Homo sapiens]  
Length = 109

Score = 195 bits (496), Expect = 2e-48

Identities = 84/106 (79%), Positives = 95/106 (89%)

Query: 425 MTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVTRTPVRGLFHLWHEKRCMDE 484

MTCQYRSDF+ IGGFD+++KGWGGEDVHLYRKYLH +LIV+RTPV GLFHLWHEKRC DE

Sbjct: 1 MTCQYRSDFLTIGGFDMEVKGWGGEDVHLYRKYLHGD LIVIRTPVPGLFHLWHEKRCDE 60

Query: 485 LTPEQYKMCQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530

LTPEQY+MC+QSKAMNEASH LGMLVFR EIE HL KQ +T+S+

Sbjct: 61 LTPEQYRMCIQSKAMNEASHSHLGMLVFREEIETHLHKQAYRTNSE 106

☐ >gi|38086850|ref|XP\_194358.2| similar to mKIAA0990 protein [Mus musculus]  
Length = 800

Score = 192 bits (488), Expect = 2e-47

Identities = 107/299 (35%), Positives = 168/299 (56%), Gaps = 21/299 (7%)

Query: 215 RTERDKGTLYELTFKGDHKHEFKRLILFR-PFSPIMKVKNELNMANTLINVIVPLAKRV 273

R +D G+L L+ + K+L+ F+ P S K E IN+++PL+ R

Sbjct: 495 RINQDSGSLSFSL-----NSLKKLVAFQLPGS-----KTEHKPEKKEKINILIPLSGRF 543

Query: 274 DKFRQFMQNFREMCIEQDGRVHLTVVYFGKE---EINEVKGILENTSKAANFRNFTFIQ 329

D F +FM NF + C+ + V L ++ F + + +V+ + + K + +

Sbjct: 544 DMFVRFMGNFEKTCCLIPNLNVKLVIILFNSDSNPDKAKQVELMRDYRVKYPK-ADMQVLP 602

Query: 330 LNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTRCLNTQPGKKVFYPVLFSSQ 389

++G FSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQ

Sbjct: 603 VSGGFSRALALEVGSSQFNES-LLFFCDVDLVFTAFLQRCRANTVLGQQIYFPIIFSQ 661

Query: 390 YNPGIIGHHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGGE 449

Y+P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG E  
 Sbjct: 662 YDPKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLE 718

Query: 450 DVHLYRKYLHNSLIVVTRTPVRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLG 508  
 DV L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL  
 Sbjct: 719 DVDLFNKVVQAGLKTFRSQEVGVVHIHPVVCDPNLDPKQYKMC LGSKASTFGSTQQLA 777

☐ >gi|37360174|dbj|BAC98065.1| mKIAA0990 protein [Mus musculus]  
 Length = 821

Score = 192 bits (488), Expect = 2e-47  
 Identities = 107/299 (35%), Positives = 168/299 (56%), Gaps = 21/299 (7%)

Query: 215 RTERDKGTLTYELTFKGDHKHEFKRLILFR-PFSPIMKVKNELNMANTLINVIVPLAKRV 273  
 R +D G+L L+ + K+L+ F+ P S K E IN+++PL+ R  
 Sbjct: 516 RINQDSGSLSLFSL-----NSLKKLVAFQLPGS-----KTEHKPEKKEKINILIPLSGRF 564

Query: 274 DKFRQFMQNFREMCIEQDGRVHLTVVYFGKE----EINEVKGILENTSKAANFRNFTFIQ 329  
 D F +FM NF + C+ + V L ++ F + + +V+ + + K + +  
 Sbjct: 565 DMFVRFMGNFEKTC LIPNLNVKL VILLFNSDSNPDKAKQVELMRDYRVKYPK-ADMQVLP 623

Query: 330 LNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQ 389  
 ++G FSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQ  
 Sbjct: 624 VSGGFSRALALEVGSSQFNNE-LLFFCDVDLVFTAFLQRCRANTVLGQQIYFPPIIFSQ 682

Query: 390 YNPGIYGHHDVAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGE 449  
 Y+P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG E  
 Sbjct: 683 YDPKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLE 739

Query: 450 DVHLYRKYLHNSLIVVTRTPVRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLG 508  
 DV L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL  
 Sbjct: 740 DVDLFNKVVQAGLKTFRSQEVGVVHIHPVVCDPNLDPKQYKMC LGSKASTFGSTQQLA 798

☐ >gi|18606381|gb|AAH23112.1| Galnact2 protein [Mus musculus]  
 Length = 109

Score = 191 bits (486), Expect = 3e-47  
 Identities = 81/106 (76%), Positives = 96/106 (90%)

Query: 425 MTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHNSLIVVTRTPVRGLFHLWHEKRCMDE 484  
 MTCQY+SDF+++GGFD+++KGWGGEDVHLYRKYLH +LIV+RTPV GLFHLWHEK C DE  
 Sbjct: 1 MTCQYQSDFLSVGGFDMEVKGWGGEDVHLYRKYLHGD L V I R T P V P G L F H L W H E K H C A D E 60

Query: 485 LTPEQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530  
 LTPEQY+MC+QSKAMNEASH LGM+VFR EIE HLRKQ +T+S+  
 Sbjct: 61 LTPEQYRMCIQSKAMNEASHSHLGMMVFREIEHMLRKQAYRTNSE 106

☐ >gi|47086685|ref|NP\_997843.1| carbohydrate (chondroitin) synthase 1; wu:fc27h0  
 gi|40352710|gb|AAH64670.1| Carbohydrate (chondroitin) synthase 1 [Danio rerio]  
 Length = 801

Score = 187 bits (475), Expect = 5e-46  
 Identities = 101/281 (35%), Positives = 159/281 (56%), Gaps = 13/281 (4%)

Query: 234 HEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGR 293  
 + K L+ F+ SP ++ K IN++VPLA R + F +FM NF ++C+ +  
 Sbjct: 507 NSLKMLVPFKLSSPGIEQHEPK---EKKINILVPLAGRYEIFLRFRMANFEKICLIPNQN 562

Query: 294 VHLTVVYFGK----EEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKG 349  
 V L ++ F E I +++ + E K + ++G FSR L+VG+ +  
 Sbjct: 563 VKLLILLFSTDNNTERIKQIELMREYRMKYPK-ADMEIKPVSGPFSRALALEVGSAHFT- 620

Query: 350 SNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYGHHDVAVPPLEQQ 409  
 ++ LLF+CDVD+ FT +FL CR NT G++ ++P++FSQY+P ++Y P +

Sbjct: 621 NDSLLFYCDVDLLFTPDFLTRCRGNTILGEQTYFPPIIFSQYDPKVVA---GKVPSDNHY 677


Query: 410 VIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLSNLIIVVTPV 469  
V +TG WR +GFG+ C Y+ D + GGFD+ I+GWG EDV L+ K++ S + + R+

Sbjct: 678 VFTSKTGLWRHYGFGIVCVYKGDVKGAGGFDVSIQGWGLEDVDLNFNKFVQSGIKLFRSTD 737

Query: 470 RGLFHLWHEKRCMDELTPSEQYKMCMSKAMNEASHGQLGML 510

G+ H+ H C L P+QYKMC+ SKA + S QL L

Sbjct: 738 TGIVHVHPVVCDPNLDPKQYKMCGLGSKASSHGSTQQLAEL 778

 >gi|47213615|emb|CAF95956.1| unnamed protein product [Tetraodon nigroviridis]  
Length = 838

Score = 186 bits (473), Expect = 9e-46

Identities = 96/252 (38%), Positives = 143/252 (56%), Gaps = 9/252 (3%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGK---EEINEVKGILENTSK 318  
+N++VPL+ R D F +FM NF +C+ + V L V+ F E + +V+ + E K

Sbjct: 570 VNILVPLSGRYDIFVRFMANFERICLIPNQNVKLLVLLFNTDNTERVKQVELMREYHMK 629

Query: 319 AANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPG 378  
+ G FSR L+VG+ + ++ LLF+CDVD+ FTSEFL CR NT G

Sbjct: 630 YPR-AEMEIRPVTGFSFRRALALEVGLHFS-NDSLLFYCDVDLLFTSEFLKRCRANTALG 687

Query: 379 KKVFPVPLFSQYNPGIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGG 438  
+ ++P++FSQY+P ++Y P V +TG WR++GFG+ C Y+ D + GG

Sbjct: 688 AQAYFPPIIFSQYDPKVVA---GKVPSNNHYVFTAKTGLWRNYGFGIVCVYKGDVLRAGG 744

Query: 439 FDLDIKGWGGEDVHLYRKYLSNLIIVVTPVRGLFHLWHEKRCMDELTPSEQYKMCMSKA 498  
FD I+GWG EDV L+ K++ S + + R+ G+ H+ H C L +QYKMC+ SKA

Sbjct: 745 FDTSIQGWGLEDVDLNFNKFVQSGIKLFRSTDGTGIVHHPVICDPNLEAKQYKMCGLSKA 804

Query: 499 MNEASHGQLGML 510

+ S QL L

Sbjct: 805 SSHGSTQQLAEL 816

 >gi|40789012|dbj|BAA76834.2| KIAA0990 protein [Homo sapiens]  
Length = 883

Score = 186 bits (473), Expect = 9e-46

Identities = 106/297 (35%), Positives = 169/297 (56%), Gaps = 17/297 (5%)

Query: 215 RTERDKGTLTYELTFKGDHKEFKRLILFRPFSPIMKVKNKLNLMANTLINVIVPLAKRVD 274  
R ++ G+L L+ + K+L+ F+ + K+E + IN+++PL+ R D

Sbjct: 577 RINQESGSLSFLS-----NSLKKLVFPQ---LPGSKSEHKEPKDKKINILIPLSGRFD 626

Query: 275 KFRQFMQNFREMCIEQDGRVHLTVVYFGKEE-INEVKGILENTSKAANF--RNFTFIQLN 331  
F +FM NF + C+ + V L V+ F + ++ K + T + + + ++

Sbjct: 627 MFVRFMGNFECTCLIPNQNVKLVLLFNSDSNPDKAKQVELMTDYRIKYPKADMQILPVS 686

Query: 332 GEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFPVPLFSQYN 391  
GEFSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQY+

Sbjct: 687 GEFSRALALEVGSSQFNNE-LLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPPIIFSQYD 745


Query: 392 PGIIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDV 451  
P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG EDV

Sbjct: 746 PKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGDVLRVGGFDVSIQGWGLEDV 802

Query: 452 HLYRKYLSNLIIVVTPVRGLFHLWHEKRCMDELTPSEQYKMCMSKAMNEASHGQLG 508

L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL

Sbjct: 803 DLFNKVVQAGLKTFRSQEVGVVHVHPVFCDPNLDPKQYKMCGLGSKASTYGSTQQLA 859

 >gi|15617453|dbj|BAB64936.1| chondroitin synthase [Homo sapiens]  
Length = 802

Score = 186 bits (472), Expect = 1e-45

Identities = 106/297 (35%), Positives = 169/297 (56%), Gaps = 17/297 (5%)

Query: 215 RTERDKGTLTYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVD 274  
 R ++ G+L L+ + K+L+ F+ + K+E + IN+++PL+ R D  
 Sbjct: 496 RINQESGSLSFLS-----NSLKKLVPFQ----LPGSKSEHKEPKDKKINILIPLSGRFD 545

Query: 275 KFRQFMQNFREMCIEQDGRVHLTVVYFGKEE-INEVKGILENTSKAANF--RNFTFIQLN 331  
 F +FM NF + C+ + V L V+ F + ++ K + T + + + ++  
 Sbjct: 546 MFVRFMGNFEKTCCLIPNQNVKLVLVLLFNSDSNPDKAKQVELMTDYRIKYPKADMQILPVS 605

Query: 332 GEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQYN 391  
 GEFSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQY+  
 Sbjct: 606 GEFSRALALEVGSSQFNNE-LLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYD 664

Query: 392 PGIIYGHHDVAPPLEQQLVIKKETGFWRDFGFGMTCCQYRSDFINIGGFDLDIKGWGGEDV 451  
 P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG EDV  
 Sbjct: 665 PKIVY---SGKVPNDNHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDV 721

Query: 452 HLYRKYLHSNLIVVRTPVRLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLG 508  
 L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL  
 Sbjct: 722 DLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLA 778

>gi|31542309|ref|NP\_055733.2| carbohydrate (chondroitin) synthase 1; chondroitin synthase [Homo sapiens]  
 gi|28279346|gb|AAH46247.1| Carbohydrate (chondroitin) synthase 1 [Homo sapiens]  
 Length = 802

Score = 185 bits (470), Expect = 2e-45

Identities = 106/298 (35%), Positives = 170/298 (57%), Gaps = 19/298 (6%)

Query: 215 RTERDKGTLTYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVD 274  
 R ++ G+L L+ + K+L+ F+ + K+E + IN+++PL+ R D  
 Sbjct: 496 RINQESGSLSFLS-----NSLKKLVPFQ----LPGSKSEHKEPKDKKINILIPLSGRFD 545

Query: 275 KFRQFMQNFREMCIEQDGRVHLTVVYFGKE---EINEVKGILENTSKAANFRNFTFIQL 330  
 F +FM NF + C+ + V L V+ F + + +V+ + + K + + +  
 Sbjct: 546 MFVRFMGNFEKTCCLIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPK-ADMQILPV 604

Query: 331 NGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQY 390  
 +GEFSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQY  
 Sbjct: 605 SGEFSRALALEVGSSQFNNE-LLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQY 663

Query: 391 NPGIIYGHHDVAPPLEQQLVIKKETGFWRDFGFGMTCCQYRSDFINIGGFDLDIKGWGGED 450  
 +P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG ED  
 Sbjct: 664 DPKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLED 720

Query: 451 VHLYRKYLHSNLIVVRTPVRLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLG 508  
 V L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL  
 Sbjct: 721 VDLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLA 778

>gi|37182181|gb|AAQ83893.1| CHSY1 [Homo sapiens]  
 Length = 802

Score = 185 bits (470), Expect = 2e-45

Identities = 106/298 (35%), Positives = 170/298 (57%), Gaps = 19/298 (6%)

Query: 215 RTERDKGTLTYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVD 274  
 R ++ G+L L+ + K+L+ F+ + K+E + IN+++PL+ R D  
 Sbjct: 496 RINQESGSLSFLS-----NSLKKLVPFQ----LPGSKSEHKEPKDKKINILIPLSGRFD 545

Query: 275 KFRQFMQNFREMCIEQDGRVHLTVVYFGKE---EINEVKGILENTSKAANFRNFTFIQL 330  
 F +FM NF + C+ + V L V+ F + + +V+ + + K + + +  
 Sbjct: 546 MFVRFMGNFEKTCCLIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPK-ADMQILPV 604

Query: 331 NGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQY 390  
+GEFSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQY  
Sbjct: 605 SGEFSRALALEVGSSQFNNES-LLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQY 663

Query: 391 NPGIIGHHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGED 450  
+P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG ED  
Sbjct: 664 DPKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLED 720

Query: 451 VHLYRKYLHSNLIVVRTPVGRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLG 508  
V L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL  
Sbjct: 721 VDLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLDPKQYKMC LGSKASTYGSTQQLA 778

☐ >gi|34357503|ref|XP\_218759.2| similar to carbohydrate (chondroitin) synthase 1  
norvegicus]  
Length = 799

Score = 183 bits (465), Expect = 7e-45  
Identities = 106/298 (35%), Positives = 168/298 (56%), Gaps = 19/298 (6%)

Query: 215 RTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVD 274  
R +D G+L L+ + K+L+ F+ M+ K K IN+++PL+ R D  
Sbjct: 495 RINQDSGSLSPLS-----NSLKKLVPPQLPGSKMEHKEPK----EKKINILIPLSGRFD 544

Query: 275 KFRQFMQNFREMCIEQDGRVHLTVVYFGKE---EINEVKGILENTSKAANFRNFTFIQL 330  
F +FM NF + C+ + V L ++ F + + +V+ + + K + + +  
Sbjct: 545 MFVRFMGNFEKTC LIPNLNVKLVILLFNSDSNPDKAKQVELMRDYRVKYPK-ADMQVLPV 603

Query: 331 NGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQY 390  
+G FSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQY  
Sbjct: 604 SGGFSRALALEVGSSQFSNES-LLFFCDVDLVFTAFLQRCRANTVLGQQIYFPIIFSQY 662

Query: 391 NPGIIGHHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGED 450  
+P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG ED  
Sbjct: 663 DPKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLED 719

Query: 451 VHLYRKYLHSNLIVVRTPVGRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLG 508  
V L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL  
Sbjct: 720 VDLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLDPKQYKMC LGSKASTFGSTQQLA 777

☐ >gi|41210270|ref|XP\_210054.3| similar to dJ341D10.1 (novel protein) [Homo sapi  
gi|17736645|emb|CAD19074.1| dJ341D10.1 (novel protein) [Homo sapiens]  
Length = 109

Score = 174 bits (442), Expect = 3e-42  
Identities = 77/106 (72%), Positives = 90/106 (84%)

Query: 425 MTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVGRGLFHLWHEKRCMDE 484  
MTCQYRSDF+ IG FD+++KGWGGEDVHL +KYLH +LIV+ TPV GLFHLW EKRC DE  
Sbjct: 1 MTCQYRSDFLIIGRFDMEVKGWGGEDVHL CQKYLHGDLIVIWTPTGLFHLWPEKRCDE 60

Query: 485 LTPEQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSK 530  
LTPEQY+MC+QSKA+NEAS LGMLVFR EIE HL KQ +T+S+  
Sbjct: 61 LTPEQYRMCIQSKAINEASRSHLGMLVFREIEIETHLHKQAYRTNSE 106

☐ >gi|48139301|ref|XP\_396991.1| similar to chondroitin synthase-like protein [Ap  
Length = 1094

Score = 174 bits (442), Expect = 3e-42  
Identities = 87/258 (33%), Positives = 146/258 (56%), Gaps = 8/258 (3%)

Query: 260 NTLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYF---GKEEINEVKGILENT 316  
+ +++ I+PL+ R + FR+F+QN+ E+C+ R L ++ + + N ++E  
Sbjct: 549 DKMVHFILPLSGRYEIFRRFLQNYEEICLTSGERTALLIMLYHHRTENSFNRTIDLVERL 608

Query: 317 SKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQ 376



+ I ++G FSR K L+ G K +N L+ F DVDI FT L R+NT  
 Sbjct: 609 KYKYRSASIDIIPISGTFSRKALNYGVSRK-LNNDLMLFIDVDIAFTESALYRIRVNTL 667  
 Query: 377 PGKKVFYPVLFSSQYNPGIIYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINI 436  
 G+++++PV+FSQY+P I+YG D P I + G+WR FGFG+ Y+ D+ ++  
 Sbjct: 668 LGRQMYFPVVFSSQYDPKIVYG--DTKSP--DTFAINEMAGYWRQFGFGIVSLYKQDYKHV 723  
 Query: 437 GGFDLDIKGWGGEDVHLYRKYLHNSLIVVPTVRGLFHLWHEKRCMDELTPQYKMCQMOS 496  
 GGF+L I+GWG EDV Y + + S++ + R + L H++H+ C +L+ Q+ MCM +  
 Sbjct: 724 GGFNLSIQGWGKEDVDFYERVIKSSIKIFRAADKDLVHVYHDVECSKDLSETQWSMCMGT 783  
 Query: 497 KAMNEASHGQLGMLVFRH 514  
 KA A L +++ +  
 Sbjct: 784 KADTLAGTETLAQMIYEN 801

☐ >gi|42662609|ref|XP\_378128.1| similar to dJ19N1.1 (novel protein) [Homo sapien]  
 gi|9863541|emb|CAC04141.1| dJ19N1.1 (novel protein) [Homo sapiens]  
 Length = 93

Score = 149 bits (375), Expect = 2e-34  
 Identities = 65/90 (72%), Positives = 76/90 (84%)

Query: 441 LDIKGWGGEDVHLYRKYLHNSLIVVPTVRGLFHLWHEKRCMDELTPQYKMCQMOSKAMN 500  
 +++KGWGGEDVHLYRKYL +LIV+R PV GLFHLWHEK C DELTPQY+MC+QSKAM+  
 Sbjct: 1 MEVKGWGGEDVHLYRKYLRGDLIVIRNPVPGFLFHLWHEKHCADELTPEQYRMCIQSKAMD 60  
 Query: 501 EASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530  
 EAS LGMLVFR EIE HL KQ +T+S+  
 Sbjct: 61 EASRSHLGMLVFREEIETHLHKQAYRTNSE 90

☐ >gi|31158517|gb|AAC85275.1| chondroitin synthase-like protein [Drosophila melanc]  
 Length = 827

Score = 136 bits (343), Expect = 1e-30  
 Identities = 85/267 (31%), Positives = 132/267 (49%), Gaps = 32/267 (11%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGK-EEINEVKGILENTSKAAN 321  
 I ++P+A R+ F +F++ + +C+ + L VV FG +E+ + +L +  
 Sbjct: 522 IVFVLPIAGRLGTFRFLRTYERVCVRGEQHCDDLVLVIFGSPDELGDHLQLLHDLHARHV 581  
 Query: 322 FRNFTFIQLNGEFSRGKGLDVGAR--FWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379  
 ++ +IQ + FSRG LDV AR + + +++LF DVD+ F E L R++TQ GK  
 Sbjct: 582 YQQVNWIIQRSSAFSRGVALDVAARSSYIRQEDIILFI-DVDMVFVEVETLQVRMHTQRGK 640  
 Query: 380 KVFPVLFSSQYNPGIIYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFI--NIG 437  
 +V+ P++FSQY+P G + I E G++R FGFG+ Y+SD + +I  
 Sbjct: 641 QVYLPVIFSSQYDPQRRSGDAGGEDEGETPRIDDERGYFRQFGFGICAIYKSDILDEDIN 700  
 Query: 438 GFDLDIKGWGGEDVHLYRKYLH-----SNLIVVPTVRG 471  
 GFD DI GWG EDV K + L V R P  
 Sbjct: 701 GFDKIDITGWGLEDDVKFLEKIVRVGTRQRGFLANTAELAMDYNEAAEQWRRLSVFRAPDPT 760  
 Query: 472 LFHLWHEKRCMDELTPQYKMCQMOSKA 498  
 L H++H+ C +L QY MC+ +KA  
 Sbjct: 761 LVHIYHDISCDVQLDAPQYNMCLGTGA 787

☐ >gi|45555191|ref|NP\_996440.1| CG9220-PC [Drosophila melanogaster]  
 gi|45446963|gb|AAS65341.1| CG9220-PC [Drosophila melanogaster]  
 Length = 863

Score = 136 bits (343), Expect = 1e-30  
 Identities = 85/267 (31%), Positives = 132/267 (49%), Gaps = 32/267 (11%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGK-EEINEVKGILENTSKAAN 321  
 I ++P+A R+ F +F++ + +C+ + L VV FG +E+ + +L +

Sbjct: 558 IVFVLPIAGRLGTFERFLRTYERVCVRGEQHCDDLVLVIFGSPDELGDHLQLLHDLHARHV 617

Query: 322 FRNFTFIQLNGEFSRGKGLDVGAR--FWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379  
++ +IQ + FSRG LDV AR + + +++LF DVD+ F E L R++TQ GK

Sbjct: 618 YQQVNWIQRSSAFSRGVALDVAARSSYIRQEDIILFI-DVDMVFEVETLQVRMHTQRGK 676

Query: 380 KVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFI--NIG 437  
+V+ P++FSQY+P G + I E G++R FGFG+ Y+SD + +I

Sbjct: 677 QVYLPVIFSQYDPQRRSGDAGGSEDEGETPRIDDERGYFRQFGFGICAIYKSDILDEDIN 736

Query: 438 GFDLDIKGWGGEDVHLYRKYLH-----SNLIVVRTPVVRG 471  
GFD DI GWG EDV K + L V R P

Sbjct: 737 GFDKDITGWGLEVDKFLKIVRVGTRQGRFLANTAEALAMYNEAAEQWRRLSVFRAPDPT 796

Query: 472 LFHLWHEKRCMDELTPQYKMCMSKA 498  
L H++H+ C +L QY MC+ +KA

Sbjct: 797 LVHIYHDISCDVQLDAPQYNMCLGTKA 823

☐ >gi|45555180|ref|NP\_996439.1| CG9220-PB [Drosophila melanogaster]  
gi|22832276|gb|AAF48479.2| CG9220-PB [Drosophila melanogaster]  
Length = 608

Score = 135 bits (341), Expect = 2e-30

Identities = 85/267 (31%), Positives = 132/267 (49%), Gaps = 32/267 (11%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGK-EEINEVKGILENTSKAAN 321  
I ++P+A R+ F +F++ + +C+ + L VV FG +E+ + +L +

Sbjct: 303 IVFVLPIAGRLGTFERFLRTYERVCVRGEQHCDDLVLVIFGSPDELGDHLQLLHDLHARHV 362

Query: 322 FRNFTFIQLNGEFSRGKGLDVGAR--FWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379  
++ +IQ + FSRG LDV AR + + +++LF DVD+ F E L R++TQ GK

Sbjct: 363 YQQVNWIQRSSAFSRGVALDVAARSSYIRQEDIILFI-DVDMVFEVETLQVRMHTQRGK 421

Query: 380 KVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFI--NIG 437  
+V+ P++FSQY+P G + I E G++R FGFG+ Y+SD + +I

Sbjct: 422 QVYLPVIFSQYDPQRRSGDAGGSEDEGETPRIDDERGYFRQFGFGICAIYKSDILDEDIN 481

Query: 438 GFDLDIKGWGGEDVHLYRKYLH-----SNLIVVRTPVVRG 471  
GFD DI GWG EDV K + L V R P

Sbjct: 482 GFDKDITGWGLEVDKFLKIVRVGTRQGRFLANTAEALAMYNEAAEQWRRLSVFRAPDPT 541

Query: 472 LFHLWHEKRCMDELTPQYKMCMSKA 498  
L H++H+ C +L QY MC+ +KA

Sbjct: 542 LVHIYHDISCDVQLDAPQYNMCLGTKA 568

☐ >gi|31158514|gb|AA085273.1| chondroitin disaccharide polymerase [Caenorhabditis]  
Length = 734

Score = 134 bits (336), Expect = 6e-30

Identities = 82/245 (33%), Positives = 134/245 (54%), Gaps = 10/245 (4%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIE--QDGRVHLTVVYFGKEEINEVKGILENTSKAA 320  
+++I+PL R F +F Q+ + +C D V LT+V + E+ E + +E A

Sbjct: 484 LHMIMPLRGAAIFARFAQHLKSICARGGDDLAVALTIVLYSSEDEMENRETIEMLR--A 541

Query: 321 NFRNFTFIQLNG-EFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379  
+F T I++ FSRG L GA +N LLFF DVD+ FT + L + NT

Sbjct: 542 SFIPVTVIEMGDVSFSRGVALMRGAETLP-ANALLFFTVDVMDLFTCDALKRIKSNTILNA 600

Query: 380 KVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGF 439  
++++P++FS+++ + +D + L + G++R FG+G+ Y++D +++GGF

Sbjct: 601 QIYFPPIVFSEFSHES-WESENKDL--LADAFHYGRGRGYFRHFGYGLAAMYKADLMDVGGF 657

Query: 440 DLDIKGWGGEDVHLYRKYL-HSNLIVVRTPVVRGLFHLWHEKRCMDELTPQYKMCMSKA 498  
D I+GWG EDV L+ K + + L V+R P GL H++H C + + Q MC SKA

Sbjct: 658 DTKIEGWGKEDVDLFEKAIAKNGRLRVIRVPEPGLVHIYHPIHCNEMPTAQKDMCHGSKA 717

Query: 499 MNEAS 503  
+ AS

Sbjct: 718 ASLAS 722

☐ >gi|31044074|dbj|BAC76780.1| chondroitin synthase [Caenorhabditis elegans]  
Length = 726

Score = 134 bits (336), Expect = 6e-30

Identities = 82/245 (33%), Positives = 134/245 (54%), Gaps = 10/245 (4%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIE--QDGRVHLTVVYFGKEEINEVKGILENTSKAA 320  
+++I+PL R F +F Q+ + +C D V LT+V + E+ E + +E A

Sbjct: 476 LHMIMPLRGAAIFARFAQHLKSICARGGDDLAVSLTIVLYSSEDEMENRETIEMLR--A 533

Query: 321 NFRNFTFIQLNG-EFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGK 379  
+F T I++ FSRG L GA +N LLFF DVD+ FT + L + NT

Sbjct: 534 SFIPVTVIEMGDVSFSRGVALMRGAETLP-ANALLFFTDVDMFLTCDALKRIKSNTILNA 592

Query: 380 KVFYPVLFSQYNPGIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGF 439  
++++P++FS+++ + +D + L + G++R FG+G+ Y++D +++GGF

Sbjct: 593 QIYFPPIVFSEFSHES-WSENDKL--LADAFHYGRGRGYFRHFGYGLAAMYKADLMDVGGF 649

Query: 440 DLDIKGWGGEDVHLYRKYL-HSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMQSKA 498  
D I+GWG EDV L+ K + + L V+R P GL H++H C + + Q MC SKA

Sbjct: 650 DTKIEGWGKEDVDLFEKAIAKNGRLRVIRVPEPGLVHIYHPIHCNEMPTAQKDMCHGSKA 709

Query: 499 MNEAS 503  
+ AS

Sbjct: 710 ASLAS 714

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Jun 23, 2004 12:06 AM

Number of letters in database: 619,474,291

Number of sequences in database: 1,866,121

Lambda K H  
0.321 0.137 0.410

Gapped  
Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 129,716,455

Number of Sequences: 1866121

Number of extensions: 5644366

Number of successful extensions: 16471

Number of sequences better than 10.0: 50

Number of HSP's better than 10.0 without gapping: 25

Number of HSP's successfully gapped in prelim test: 25

Number of HSP's that attempted gapping in prelim test: 16391

Number of HSP's gapped (non-prelim): 65

length of query: 532

length of database: 619,474,291

effective HSP length: 130

effective length of query: 402

effective length of database: 376,878,561  
effective search space: 151505181522  
effective search space used: 151505181522  
T: 11  
A: 40  
X1: 16 ( 7.4 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 41 (21.8 bits)  
S2: 76 (33.9 bits)